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OM nucleic - nucleic search, using sw model

Run on: April 21, 2006, 08:53:52 ; Search time 1606 Seconds  
(without alignments)  
11302.170 Million cell updates/sec

Title: US-10-541-315-1

Perfect score: 2195  
Sequence: 1 aatccgaaagttctgcac.....cacttcaccagcaagttc 2195

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA\_Main:\*

- 1: /cgn2\_6/prodata/1/pubpna/US07\_PUBCONB.seq:\*
- 2: /cgn2\_6/prodata/1/pubpna/US08\_PUBCONB.seq:\*
- 3: /cgn2\_6/prodata/1/pubpna/US09A\_PUBCONB.seq:\*
- 4: /cgn2\_6/prodata/1/pubpna/US09B\_PUBCONB.seq:\*
- 5: /cgn2\_6/prodata/1/pubpna/US10A\_PUBCONB.seq:\*
- 6: /cgn2\_6/prodata/1/pubpna/US10B\_PUBCONB.seq:\*
- 7: /cgn2\_6/prodata/1/pubpna/US10C\_PUBCONB.seq:\*
- 8: /cgn2\_6/prodata/1/pubpna/US10D\_PUBCONB.seq:\*
- 9: /cgn2\_6/prodata/1/pubpna/US10E\_PUBCONB.seq:\*
- 10: /cgn2\_6/prodata/1/pubpna/US11\_PUBCONB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	867.2	39.5	898	5	US-10-011-672-35 Sequence 35, Appl
2	867.2	39.5	898	5	US-10-012-070A-50 Sequence 50, Appl
3	682.6	31.1	762	7	US-10-437-963-33718 Sequence 33718, A
4	136.8	3.1	3221	7	US-10-437-963-7912 Sequence 7912, Ap
5	126.8	5.8	725	9	US-10-487-901-2760 Sequence 2760, Ap
6	126.8	5.8	725	9	US-10-487-901-6610 Sequence 6610, Ap
7	126.8	5.8	808	7	US-10-260-238-51 Sequence 51, Appl
8	120.2	3.8	781	7	US-10-437-963-7907 Sequence 7907, Ap
9	84.2	3.8	195	7	US-10-437-963-79997 Sequence 79997, A
10	77.4	3.5	294	7	US-10-437-963-49995 Sequence 49995, A
11	64.4	2.9	165	7	US-10-437-963-10222 Sequence 10222, A
12	59.6	2.7	213	7	US-10-437-963-54806 Sequence 54806, A
13	55.6	2.5	101954	7	US-10-322-281-782 Sequence 782, App
14	55.4	2.5	8056	8	US-10-473-126-386 Sequence 386, App
15	55.4	2.5	367378	6	US-10-312-841-1 Sequence 1, Appl
16	55.2	2.5	5379	6	US-10-311-455-1649 Sequence 1649, Ap
17	55.2	2.5	5379	6	US-10-240-485-129 Sequence 129, App
18	55	2.5	69081	5	US-10-087-192-1132 Sequence 1192, Ap
19	54.4	2.5	16766	6	US-10-311-455-2129 Sequence 2129, Ap
20	53.8	2.5	9760	7	US-10-221-613-113 Sequence 113, App
21	53	2.4	1243	8	US-10-425-115-17217 Sequence 17217, A
22	52.6	2.4	8076	7	US-10-257-166-36 Sequence 36, Appl
23	52.6	2.4	8136	6	US-10-311-455-528 Sequence 528, App

C	24	52.6	2.4	8136	7	US-10-257-166-38	Sequence 38, Appl
C	25	52.6	2.4	158001	7	US-10-211-179-11	GENERAL INFORMATION
C	26	52.4	2.4	3673778	6	US-10-312-841-1	Sequence 1, Appl
C	27	51.6	2.4	8056	8	US-10-473-126-240	Sequence 240, App
C	28	51.6	2.4	147300	9	US-10-723-681-3	Sequence 3, Appl
C	29	51.4	2.3	5979	5	US-10-239-676-18	Sequence 18, Appl
C	30	51.4	2.3	5979	5	US-10-240-453-26	Sequence 26, Appl
C	31	51.4	2.3	7941	7	US-10-433-793-139	Sequence 139, App
C	32	51.2	2.3	998	3	US-09-816-894-5	Sequence 5, Appl
C	33	51.2	2.3	7374	7	US-10-257-166-117	Sequence 117, App
C	34	51	2.3	14095	6	US-10-311-455-450	Sequence 450, App
C	35	50.8	2.3	15732	5	US-10-239-676-95	Sequence 95, Appl
C	36	50.8	2.3	15732	6	US-10-240-453-107	Sequence 107, App
C	37	50.6	2.3	6131	6	US-10-311-455-863	Sequence 863, App
C	38	50.2	2.3	16766	6	US-10-311-455-2130	Sequence 2130, Ap
C	39	50.2	2.3	50000	8	US-10-706-635-24	Sequence 24, Appl
C	40	50	2.3	7001	5	US-10-172-086-60	Sequence 60, Appl
C	41	50	2.3	7001	7	US-10-311-507-2	Sequence 2, Appl
C	42	50	2.3	7001	8	US-10-480-846-60	Sequence 60, Appl
C	43	50	2.3	7276	6	US-10-311-455-875	Sequence 875, App
C	44	50	2.3	14006	6	US-10-311-455-1931	Sequence 1931, Ap
C	45	50	2.3	18683	6	US-10-311-455-285	Sequence 285, App

ALIGNMENTS

RESULT 1  
US-10-011-672-35

; Sequence 35, Application US/10011672  
; Publication No. US20030049814A1  
; GENERAL INFORMATION:  
; APPLICANT: Hawker, Timothy  
; APPLICANT: Warner, Simon  
; APPLICANT: Andrews, Christopher  
; APPLICANT: Bachoo, Savinder  
; APPLICANT: Pickett, Andrew  
; TITLE OF INVENTION: HERBICIDE RESISTANT PLANTS  
; FILE REFERENCE: 50489/UST  
; CURRENT APPLICATION NUMBER: US/10/011,672  
; PRIOR APPLICATION NUMBER: 2001-10-29  
; PRIOR FILING DATE: 2000-04-20  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 35  
; LENGTH: 898  
; TYPE: DNA  
; ORGANISM: Oryza sp.  
US-10-011-672-35

Query Match	39.5%	Score 867.2	DB 5	Length 898
Best Local Similarity	99.2%	Pred. No. 8.6e-186		
Matches 893	Conservative	0	Mismatches 3	Indels 4
			Gaps	2
1	AATCGGAAAGTTTGACCGTTTTCAGCTCTAATAACATATAGGAAAGTGTGCT	60		
2	AATCGGAAAGTTTGACCGTTTTCAGCTCTAATAACATATAGGAAAGTGTGCT	61		
61	AAATATTAATGAGACCTTATATATGACGCTGATTAAGAACTATATGAAGAAACT	120		
62	AAATATTAATGAGACCTTATATATGACGCTGATTAAGAACTATATGAAGAAACT	121		
121	CATTCACCTACTTGTGCGCATCGGGCTAATTAAGAAAGTGTGCTAGTTTGT	180		
122	CATTCACCTACTTGTGCGCATCGGGCTAATTAAGAAAGTGTGCTAGTTTGT	181		
181	TTTCCCTTATTAATGAGGAAATGAATCATTTGCTTGAATATACCTTACATC	240		
182	TTTCCCTTATTAATGAGGAAATGAATCATTTGCTTGAATATACCTTACATC	241		
241	TTTGTGATGAGTAAATTTTGTGAGGTGCAATATTTGTCATCAAACTCTTGTGATTA	300		

Db 242 TCTGTCATGAAGTTAAATTAATTCGAGTACGCCATTAATGTCATCAAACTCTTCTTGAAAT 301  
 Qy 301 AAAAAATCTTCTAGCTGAAGTCAATGGGTAAAGAGATATTTTAAAAAATAAT 360  
 Db 302 AAAAAATCTTCTAGCTGAAGTCAATGGGTAAAGAGATATTTTAAAAAATAAT 358  
 Qy 361 AGAATGAGATATTTCTGAAGTCAATGGGTAAAGAGATATTTTAAAAAATAAT 420  
 Db 359 AGAATGAGATATTTCTGAAGTCAATGGGTAAAGAGATATTTTAAAAAATAAT 418  
 Qy 421 AGTTGTGATTCGTATATTCGAGTCAATGGGTAAAGAGATATTTTAAAAAATAAT 480  
 Db 419 AGTTGTGATTCGTATATTCGAGTCAATGGGTAAAGAGATATTTTAAAAAATAAT 478  
 Qy 481 TATTTAGTATTAAGACATTAATTTTATTTATTTATTTTATTTTATTTTATTTAT 540  
 Db 479 TATTTAGTATTAAGACATTAATTTTATTTATTTATTTATTTTATTTTATTTAT 538  
 Qy 541 AAGGTACTTACGACACACTTGTGCTCATGTGCAATGTGAGTGCACCTCTC-ATACA 599  
 Db 539 AAGGTACTTACGACACACTTGTGCTCATGTGCAATGTGAGTGCACCTCTC-ATACA 598  
 Qy 600 CGTTCAACTAGGACACATCTCAATATGACCTGCTATTTATTTATTTATTTATTTAT 659  
 Db 599 CGTTCAACTAGGACACATCTCAATATGACCTGCTATTTATTTATTTATTTATTTAT 658  
 Qy 660 ATCTGAATTTCAAGCACTTCAACATCAGACACCACTTTTAAATATCAATAACAAA 719  
 Db 659 ATCTGAATTTCAAGCACTTCAACATCAGACACCACTTTTAAATATCAATAACAAA 718  
 Qy 720 AATTAATTTTACAGATAGATGAAAAAGTAAAGCACTATTTAGTTTTCACATACA 779  
 Db 719 AATTAATTTTACAGATAGATGAAAAAGTAAAGCACTATTTAGTTTTCACATACA 778  
 Qy 780 AAAAAAATTTTGTGCTGCGCGGAGCGGCATCTCCATTTTGGGACACAGGCA 839  
 Db 779 AAAAAAATTTTGTGCTGCGCGGAGCGGCATCTCCATTTTGGGACACAGGCA 838  
 Qy 840 ACAACAGATGGCTGCCACAGAACCAACCAAAAAAGATGATTAACGAGAGACAGC 899  
 Db 839 ACAACAGATGGCTGCCACAGAACCAACCAAAAAAGATGATTAACGAGAGACAGC 898

RESULT 2  
 US-10-012-070A-50  
 ; Sequence 50, Application US/10012070A  
 ; Publication No. US20030077801A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hawke, Timothy  
 ; APPLICANT: Warner, Simon  
 ; APPLICANT: Andrews, Christopher  
 ; APPLICANT: Bachoo, Savinder  
 ; APPLICANT: Pickering, Andrew  
 ; TITLE OF INVENTION: Herbicide Resistant Plants  
 ; FILE REFERENCE: 50490/US  
 ; CURRENT APPLICATION NUMBER: US/10/012,070A  
 ; CURRENT FILING DATE: 2001-10-29  
 ; PRIOR APPLICATION NUMBER: PCT/GB00/01573  
 ; PRIOR FILING DATE: 2000-04-20  
 ; NUMBER OF SEQ ID NOS: 57  
 ; SOFTWARE: Patent Ver. 2.0  
 ; SEQ ID NO 50  
 ; LENGTH: 898  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sp.  
 US-10-012-070A-50

Query Match 39.5%; Score 867.2; DB 5; Length 898;  
 Best Local Similarity 99.2%; Pred. No. 8.6e-186;  
 Matches 893; Conservative 0; Mismatches 3; Indels 4; Gaps 2;  
 Qy 1 AATCGAAAAAGTTTGTGACCGTTTACGTCCTTAACATATATGGGAAGTGTGCT 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 AATCGAAAAAGTTTGTGACCGTTTACGTCCTTAACATATATGGGAAGTGTGCT 60

Db 2 AATCGAAAAAGTTTGTGACCGTTTACGTCCTTAACATATATGGGAAGTGTGCT 61  
 Qy 61 AATATTAATTAAGACCTTATATATATGACGCTGATAAATAAGATATGTAAGAAAACT 120  
 Db 62 AATATTAATTAAGACCTTATATATATGACGCTGATAAATAAGATATGTAAGAAAACT 121  
 Qy 121 CATTCACCTTACTTTAGTGGCAATCGGGCTAAATATAAAGAGTGGCTACACTAGTTTGT 180  
 Db 122 CATTCACCTTACTTTAGTGGCAATCGGGCTAAATATAAAGAGTGGCTACACTAGTTTGT 181  
 Qy 181 TTTCCTTGAATTAAGTGGGAAAAATGAATCATATTTGCTTGAATATATGATGACATC 240  
 Db 182 TTTCCTTGAATTAAGTGGGAAAAATGAATCATATTTGCTTGAATATATGATGACATC 241  
 Qy 241 TCTGTCATGAAGTTAAATTAATTCGAGTACGCCATTAATGTCATCAAACTCTTGAATA 300  
 Db 242 TCTGTCATGAAGTTAAATTAATTCGAGTACGCCATTAATGTCATCAAACTCTTGAATA 301  
 Qy 301 AAAAAATCTTCTAGCTGAAGTCAATGGGTAAAGAGATATTTTAAAAAATAAT 360  
 Db 302 AAAAAATCTTCTAGCTGAAGTCAATGGGTAAAGAGATATTTTAAAAAATAAT 358  
 Qy 361 AGAATGAGATATTTCTGAAGTCAATGGGTAAAGAGATATTTTAAAAAATAAT 420  
 Db 359 AGAATGAGATATTTCTGAAGTCAATGGGTAAAGAGATATTTTAAAAAATAAT 418  
 Qy 421 AGTTGTGATTCGTATATTCGAGTCAATGGGTAAAGAGATATTTTAAAAAATAAT 480  
 Db 419 AGTTGTGATTCGTATATTCGAGTCAATGGGTAAAGAGATATTTTAAAAAATAAT 478  
 Qy 481 TATTTAGTATTAAGACATTAATTTTATTTATTTATTTTATTTTATTTTATTTAT 540  
 Db 479 TATTTAGTATTAAGACATTAATTTTATTTATTTATTTTATTTTATTTTATTTAT 538  
 Qy 541 AAGGTACTTACGACACACTTGTGCTCATGTGCAATGTGAGTGCACCTCTC-ATACA 599  
 Db 539 AAGGTACTTACGACACACTTGTGCTCATGTGCAATGTGAGTGCACCTCTC-ATACA 598  
 Qy 600 CGTTCAACTAGGACACATCTCAATATGACCTGCTATTTATTTATTTATTTATTTAT 659  
 Db 599 CGTTCAACTAGGACACATCTCAATATGACCTGCTATTTATTTATTTATTTATTTAT 658  
 Qy 660 ATCTGAATTTCAAGCACTTCAACATCAGACACCACTTTTAAATATCAATAACAAA 719  
 Db 659 ATCTGAATTTCAAGCACTTCAACATCAGACACCACTTTTAAATATCAATAACAAA 718  
 Qy 720 AATTAATTTTACAGATAGATGAAAAAGTAAAGCACTATTTAGTTTTCACATACA 779  
 Db 719 AATTAATTTTACAGATAGATGAAAAAGTAAAGCACTATTTAGTTTTCACATACA 778  
 Qy 780 AAAAAAATTTTGTGCTGCGCGGAGCGGCATCTCCATTTTGGGACACAGGCA 839  
 Db 779 AAAAAAATTTTGTGCTGCGCGGAGCGGCATCTCCATTTTGGGACACAGGCA 838  
 Qy 840 ACAACAGATGGCTGCCACAGAACCAACCAAAAAAGATGATTAACGAGAGACAGC 899  
 Db 839 ACAACAGATGGCTGCCACAGAACCAACCAAAAAAGATGATTAACGAGAGACAGC 898

RESULT 3  
 US-10-437-963-33718  
 ; Sequence 33718, Application US/10437963  
 ; Publication No. US20040123341  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
;; FILE REFERENCE: 38-21(53221) B  
;; CURRENT APPLICATION NUMBER: US/10/437,963  
;; CURRENT FILING DATE: 2003-05-14  
;; NUMBER OF SEQ ID NOS: 204966  
;; SEQ ID NO 33718  
;; LENGTH: 762  
;; TYPE: DNA  
;; ORGANISM: Oryza sativa  
;; FEATURE:  
;; NAME/KEY: unsure  
;; LOCATION: (1)..(762)  
;; OTHER INFORMATION: unsure at all n locations  
;; FEATURE:  
;; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_37802C.1  
US-10-437-963-33718

Query Match 31.1%; Score 682.6; DB 7; Length 762;  
Best Local Similarity 97.6%; Pred. No. 5.2e-144;  
Matches 745; Conservative 0; Mismatches 11; Indels 7; Gaps 5;

QY 1036 CCAAGAGAGGAGACACCAAGACACGAGCTAGACAGAGCGGAGCGGCTTCTT 1095  
DB 4 CAGAGAGAGGAGACACCAAGACACGAGCTAGACAGAGCGGAGCGGCTTCTT 62  
QY 1096 CGATCCATATCTTCCGGTCGAGTTCTTGTCATCTCTTCCCTCTCACTCTCTCA 1155  
DB 63 CGATCCATATCTTCCGGTCGAGTTCTTGTCATCTCTTCCCTCTCACTCTCTCA 122  
QY 1156 CAGGGATATG--CCCTTCGGTGTCTTCTGATTTATTTAGTTGTGTAGTACG 1212  
DB 123 CAGGGATATGCTCTCCCTTCGGTGTCTTCTGATTTCTTGTCTAGTTGTGTAGTACG 182  
QY 1213 GGGTGAATGTATGGAAGGGGATCTGATCTGATGATTCCTGCTCTTGATTTGGGAT 1272  
DB 183 GCTTATATGTATGGAAGGGGATCTGATCTGATGATTCCTGCTCTTGATTTGGGAT 242  
QY 1273 AGAGGGGTTCTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTCAAT 1332  
DB 243 AGAGGGGTTCTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTCAAT 302  
QY 1333 CGTCTGAGAGCTCTATGGAATGAATGGTTTAAAGGTAACGGAATCTTGCAATTTTGTGA 1392  
DB 303 CGTCTGAGAGCTCTATGGAATGAATGGTTTAAAGGTAACGGAATCTTGCAATTTTGTGA 362  
QY 1393 GATACCTTTGTTGAGTTAAATCAGAGCACCGGTATTTTGTGTTGTTAAATGAATGA 1452  
DB 363 GATACCTTTGTTGAGTTAAATCAGAGCACCGGTATTTTGTGTTGTTAAATGAATGA 421  
QY 1453 CATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1512  
DB 422 CATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 481  
QY 1513 TTTATTCCTATTTGAACAAATAATCAACTTTGAAGACGGTCCGTTGATGATGATGA 1572  
DB 482 TTTATTCCTATTTGAACAAATAATCAACTTTGAAGACGGTCCGTTGATGATGATGA 541  
QY 1573 ATGATGATTTCTTAAGCTCTGCAAAATTTGCAAGCTGGCTTTGATGATGATGATG 1632  
DB 542 ATGATGATTTCTTAAGCTCTGCAAAATTTGCAAGCTGGCTTTGATGATGATGATG 601  
QY 1633 CCATCAGAAATTCATGAAGAAAGATATATCTCTGAGAAACGGGGATCCCGTTCTTC 1692  
DB 602 CCATCAGAAATTCATGAAGAAAGATATATCTCTGAGAAACGGGGATCCCGTTCTTC 661  
QY 1693 CGATTTGCTTATGTTCCAGAAATTTTTCCTCAATATCTTAAAGATCACTTCTGAT 1752  
DB 662 CGATTTGCTTATGTTCCAGAAATTTTTCCTCAATATCTTAAAGATCACTTCTGAT 720  
QY 1753 CAGTTCAATGAATGATTTGCTACAAATATATCTTTATATGCGT 1795  
DB 721 CAGTTCAATGAATGATTTGCTACAAATATATCTTTATATGCGT 762

RESULT 4  
US-10-437-963-7912  
; Sequence 7912, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221) B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 7912  
; LENGTH: 3221  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_14463C.1  
US-10-437-963-7912

Query Match 6.2%; Score 136.8; DB 7; Length 3221;  
Best Local Similarity 89.8%; Pred. No. 4.7e-20;  
Matches 158; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 988 TATAATTCCTCCCTCTTCCCTCTCTATATATGAGGATTCAGGCAAGAGAGG 1047  
DB 221 TAAATATCTGGGTCTCACTCTCCCTCCGATATAGAGGATTCAGGCAAGAGAGG 280  
QY 1048 AGAGCACCAAGACACGCGACTAGAGAGAGCGAGCGAGCGGCTTCTTGATTCATATCT 1107  
DB 281 AGAGCACCAAGACACGCGACTAGAGAGAGCGAGCGAGCGGCTTCTTGATTCATATCT 339  
QY 1108 TCCGTTGAGTTCTTGTGATCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1163  
DB 340 TCCGTTGAGTTCTTGTGATCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 395

RESULT 5  
US-10-487-901-2760  
; Sequence 2760, Application US/10487901  
; Publication No. US20050091708A1  
; GENERAL INFORMATION:  
; APPLICANT: Oreido, Jeremiah Vincent  
; APPLICANT: McCreary, David  
; APPLICANT: Pell, Randy  
; APPLICANT: Miller, Barbara  
; APPLICANT: Weglarz, Thadeus  
; APPLICANT: Gachotte, Daniel  
; APPLICANT: Blakeslee, Beth  
; APPLICANT: Larrinus, Ignacio  
; APPLICANT: Reddy, Avutu  
; APPLICANT: Shukla, Vipula  
; APPLICANT: Crooley, Rodney  
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri  
; FILE REFERENCE: DOW-08552  
; CURRENT APPLICATION NUMBER: US/10/487,901  
; CURRENT FILING DATE: 2004-02-26  
; NUMBER OF SEQ ID NOS: 7560  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2760  
; LENGTH: 719  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic





```

: APPLICANT: Barbazuk, Brad
: TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(53221)B
: CURRENT APPLICATION NUMBER: US/10/437,963
: CURRENT FILING DATE: 2003-05-14
: NUMBER OF SEQ ID NOS: 204966
: SEQ ID NO 48995
: LENGTH: 294
: TYPE: DNA
: ORGANISM: Oryza sativa
: FEATURES:
: NAME/KEY: unsure
: LOCATION: (1)..(294)
: OTHER INFORMATION: unsure at all n locations
: FEATURES:
: OTHER INFORMATION: Clone ID: PAT_MRT4530_52525C.1
US-10-437-963-49995

Query Match      3.5%; Score 77.4; DB 7; Length 294;
Best Local Similarity 87.6%; Pred. No. 3.9e-07;
Matches 92; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Oy      1059 GACACGCGACTTACACAGAGCCGAGCGCGCTTCTTGATCATCATATCTTCGGTGCAGT 1118
Db      7 GCGACGCGACTTACACAGAGCCGAGCGCGCGC-TCCTGATCATCATATCTTCGGGCGAGT 65

Oy      1119 TCTTGTGCGATCTCTTCCCTCCCTCCACCTCTCTCTCACAGGGTAT 1163
Db      66 TCTTGTGCGATCTCTTCCCTCCCTCCACCTCTCTCTCACAGGTTCT 110

RESULT 11
US-10-437-963-10222
: Sequence 10222 : Application US/10437963
: Publication No. US20040123343A1
: GENERAL INFORMATION:
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Kovalic, David K.
: APPLICANT: Zhou, Yihua
: APPLICANT: Cao, Yongwei
: APPLICANT: Wu, Wei
: APPLICANT: Boukharov, Andrey A.
: APPLICANT: Barbazuk, Brad
: APPLICANT: Li, Ping
: TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(53221)B
: CURRENT APPLICATION NUMBER: US/10/437,963
: CURRENT FILING DATE: 2003-05-14
: NUMBER OF SEQ ID NOS: 204966
: SEQ ID NO 10222
: LENGTH: 165
: TYPE: DNA
: ORGANISM: Oryza sativa
: FEATURES:
: OTHER INFORMATION: Clone ID: PAT_MRT4530_16565C.1
US-10-437-963-10222

Query Match      2.9%; Score 64.4; DB 7; Length 165;
Best Local Similarity 80.0%; Pred. No. 0.00026;
Matches 88; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

Oy      1054 CCAAGGACGCGGACGACGAGGAGGCGGCGCGCTTCTTGATCATCATATCTTCGGGT 1113
Db      5 CAAAGGACGCTCACTACGATTAAGCGGATCGACCGCTTTC-TGATTCATATCTTCGGGT 63

Oy      1114 CGAGTCTTGTGATCTCTTCCCTCCCTCCACCTCTCTCTCACAGGGTAT 1163
Db      64 CGAGTCTTGTGATCTCTTCCCTCCCTCACTATTCACCTATTCACAGGTTT 113

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DB      6717 TAAATCAACATTAAAAACATAAAAAATTTATTTTTTAAATTAATTAATAAAATT 6658
QY      690 ACCACTTTTAAATATCTAAAAATACAAAAATATATTTTACAGATATGATGAAGATAT 749
        |||||
DB      6657 AAAAATTTCAATAAAAACATAAAAATATAACATPAAATATATAATTAATAAATAATA 6598
QY      750 GAAACGAACTATTAGCTTTTTCACATACAAAAAAAAGAAATTTT 796
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DB      6597 ATAAATTTTTCATTATTAATTTAAATTAATAATTAATAATATAT 6551
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## RESULT 15

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US-10-312-841-1
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: EpiGenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1
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Query Match      2.5%; Score 55.4; DB 6; Length 3673778;
Best Local Similarity 53.7%; Pred. No. 4.8; Indels 2; Gaps 1;
Matches 137; Conservative 0; Mismatches 116;

QY      327 GGGTAAAGAGATATTTTTTTTTTAAAAAATAGATGAGATATCTGAACTATCG 386
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DB      2720210 GGTAAATAGAGCGAGATTTATTTTAAAAAAGAAATATTTGTTTTTTT 2720269
QY      387 GCAAAGATTAAACATATATATATATTTTATAGTTTGCATTCGTTATATCGCAG 446
        |||||
DB      2720270 TTAATAGTTTAA--GTTTACGGTATATGTATACGTAGTTGTTATATATAT 2720327
QY      447 TCATTAAAGSACATGCTTACTCATCTCAATTTTATTTAGTAATTAAGACATGACT 506
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DB      2720328 AATATGTTACGTGTGTGTATTTTAAATTTTATTAATTAATTAATTTT 2720387
QY      507 TATTTTATTTATTTATCTTTTTCGATTAATGACAGTACTTACGCACACTTTGTGC 566
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DB      2720448 TTTTGTGTTATGTG 2720462
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Search completed: April 21, 2006, 09:26:22  
Job time : 1614 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 21, 2006, 08:53:44 ; Search time 7876 Seconds  
(without alignments)  
13039.315 Million cell updates/sec

Title: US-10-541-315-1  
Perfect score: 2195  
Sequence: 1 aatccgaagaagttcttcacac.....catttcaccagcaagttc 2195

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hic:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gest1:\*  
10: gb\_gest2:\*  
11: gb\_gest3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	723.4	33.0	894	10 AG832683	AG832683 Oryza sat
2	642.8	29.3	716	1 AU075848	AU075848 AU075848
3	575	26.2	627	6 CF304337	CF304337 ABP1--04-
4	566.8	25.8	619	6 CF306344	CF306344 HDAL--03-
5	531	24.2	585	7 CF303803	CF303803 41717rslc
6	526	24.0	578	6 CF303311	CF303311 ABP1--01-
c 7	479.8	21.9	775	9 AG871933	AG871933 tne0045B
8	300	13.7	848	10 AG871481	AG871481 Oryza sat
9	286.2	13.0	324	6 CF305170	CF305170 ABP1--05-
10	248.6	11.3	288	6 CF304743	CF304743 ABP1--06-
11	204.2	9.3	239	7 CF3042297	CF3042297 43579rslc
12	201.8	9.2	844	7 CF3031032	CF3031032 CR291032
13	186.8	8.5	982	5 BX929024	BX929024 BX929024
14	181.4	8.3	479	6 CF278393	CF278393 14ETL--04
15	181.4	8.3	571	6 CB214615	CB214615 OML04895
16	174.8	8.0	210	7 CF993308	CF993308 18211rslc
17	133.2	6.1	295	7 CF731585	CF731585 FLO--05-K
18	129.2	5.9	472	7 CV733575	CV733575 FLO--08-T
19	129.2	5.9	539	7 CV724966	CV724966 14Salc--0
20	129.2	5.9	550	6 CF280385	CF280385 14ETL--07
21	129.2	5.9	550	6 CF280540	CF280540 14ETL--07
22	129.2	5.9	552	6 CF319604	CF319604 HD--10-C1

23	129.2	5.9	559	6 CF277809	CF277809 14ETL--03
24	129.2	5.9	563	6 CF309066	CF309066 ABP--03-B
25	129.2	5.9	564	6 CF278675	CF278675 14ETL--04
26	129.2	5.9	565	6 CF315243	CF315243 HD--04-B1
27	129.2	5.9	566	6 CF281181	CF281181 14ETL--08
28	129.2	5.9	566	6 CF321214	CF321214 HD--12-G0
29	129.2	5.9	567	6 CF307781	CF307781 ABP--01-F
30	129.2	5.9	624	6 CF319251	CF319251 HD--09-L0
31	129.2	5.9	677	6 CF339901	CF339901 RCL1--06-
32	129.2	5.9	680	6 CF328175	CF328175 NACL--02-
33	128.8	5.9	557	6 CF340566	CF340566 RCL1--08-
34	128.8	5.9	560	6 CF338527	CF338527 RCL1--01-
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37	127.6	5.8	465	6 CF278096	CF278096 14ETL--03
38	127.6	5.8	467	6 CF281638	CF281638 14ETL--08
39	127.6	5.8	495	6 CF281318	CF281318 14ETL--08
40	127.6	5.8	496	6 CF280246	CF280246 14ETL--06
41	127.6	5.8	567	6 CF281111	CF281111 14ETL--08
42	127.6	5.8	575	6 CF278509	CF278509 14ETL--04
43	127.6	5.8	577	6 CF279802	CF279802 14ETL--06
44	127.6	5.8	580	6 CF318434	CF318434 HD--08-I2
45	127.6	5.8	586	6 CF278083	CF278083 14ETL--03

## ALIGNMENTS

RESULT 1  
AG832683/c AG832683 894 bp DNA linear GSS 03-NOV-2004  
LOCUS  
DEFINITION  
BAC clone:K0010A06\_F, genomic survey sequence.

ACCESSION  
AG832683.1 GI:55298918  
VERSION  
GSS.  
KEYWORDS  
Oryza sativa (indica cultivar-group)  
Oryza sativa (indica cultivar-group)  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
1 Katagiri, S., Wu, J., Ito, Y., Karasawa, W., Shibata, M., Kanamori, H.,  
Katayose, Y., Namiki, N., Matsumoto, T. and Sasaki, T.  
End Sequencing and Chromosomal in silico Mapping of BAC Clones  
Derived from an indica Rice Cultivar, Kasalath  
Breeding Science 54, 273-279 (2004)  
2 (bases 1 to 894)

JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Submitted (29-Oct-2004) Takuji Sasaki, National Institute of  
Direct Submission  
Sasaki, T., Matsumoto, T. and Wu, J.

COMMENT  
FEATURES  
source  
1.894  
/organism="Oryza sativa (indica cultivar-group)"  
/mol\_type="genomic DNA"  
/cultivar="Kasalath"  
/db\_xref="taxon:39946"  
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ORIGIN  
Query Match  
Best Local Similarity 97.7%; Pred. No. 6.8e-151;  
Matches 767; Conservative 0; Mismatches 11; Indels 7; Gaps 3;

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1471 TTCTGTAGTATGATCTTTCGATTTGACAGAGCTATCTTTGTTATTCCTATTGAACA 1530  
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834 TTCTGTAGTATGATCTTCCGATTTGACAGAGCTATCTTTGTTATTCCTATTGAACA 775  
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1531 AAAATTAATCACTTTGAAGACGGTCCCGTGTATGATTTGAATGATTAATCTTAAG-C 1589  
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774 AAAATTAATCACTTTGAAGACGGTCCCGTGTATGATTTGAATGATTAATCTTAAGCC 715  
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1590 CTGTCCAAATTTTCGAGCTGTGCTTTTATGATACAGTATCCCATCAAGAAATTCAG 1649  
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714 CTGTCCAAATTTTCGAGCTGTGCTTTTATGATACAGTATCCCATCAAGAAATTCAG 655  
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1650 AAAACGTTATTAATCTCTCAGGAAACAGGGATTCCTGTTCTTCCGATTTGCTTAAGTCCC 1709  
654 GAAACGTTATTAATCTCTCAGGAA-----AATCCGTTCTTCCGATTTGCTTAAGTCCC 600  
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1710 AGAATTTTTCCTCCCAATTAATCTTAATAAGTCACTTTGCTGTACCTCAATGAATGAT 1769  
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1770 TGTCTAAATTAATGCTTTTATAGCGTTATCTAGCTGTAGTTCAGTTTATAGTATATAC 1829  
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1830 CCTATAGTTTATGTCAGAGAGAACTTATCCGATTTCTGATCTCAATTTTAATTAATG 1889  
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2130 TGTCTTAATGATTAATCTTCTTGTGACAGTCTTGTGATGATTTGACATTTCAAGCA 2189  
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2190 AAGTT 2194  
119 AAGTT 115  
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RESULT 2  
LOCUS A0075848 716 bp mRNA linear EST 03-APR-2002  
DEFINITION A0075848 Rice mature leaf Oryza sativa (japonica cultivar-group)  
CDNA clone S20385\_1A, mRNA sequence.  
A0075848  
VERSION A0075848.1 GI:5455455  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriocaridaceae; Oryzaceae; Oryza.  
1 (bases 1 to 716)  
Yamamoto, K. and Sasaki, T.  
Rice cDNA from mature leaf  
Unpublished (1999)  
Contact: Takuji Sasaki  
National Institute of Agrobiological Resources  
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki

305-8602, Japan  
Tel.: 81-298-38-7441  
Fax: 81-298-38-7468  
Email: tcsasaki@abr.affrc.go.jp, URL: http://kyp.dna.affrc.go.jp/  
PROJECT = "RGP".  
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Query Match 29.3%; Score 642.8; DB 1; Length 716;  
Best Local Similarity 97.8%; Pred No. 7.2e-133;  
Matches 704; Conservative 0; Mismatches 9; Indels 7; Gaps 5;  
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1079 CGAGGACCGCCCTTTCGATCATAATCTTCGGTCGAGTCTTGATCTCTCCCT 1138  
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1139 CTTCACTCTCTCTCAAGGGTATG---CCCTTCGGTGTCTTGATTTATTTTC 1195  
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1196 TAGGTTGATGATGACGGCGTTGATTTAGAAAGGGGATCTGATCTGATGATTCCT 1255  
120 TAGGTTGATGATGACGGCGTTGATTTAGAAAGGGGATCTGATCTGATGATTCCT 179  
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1256 GTTCTGGAATTTGGATTAAGAGGGGTTCTGATGTTGATTAATGATTCGATTTGATTA 1315  
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1316 GTAGTATGATTTCAATGCTCTGAGAGACTCTATAGGAAATGAATAGCTTTAGGGATCGA 1375  
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1376 ATCTTGCAATTTTGAGAGACCTTTGTTGAGGTAATCAGACACCGGATTTTGC 1435  
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1436 TTGGTATTAATAAGTACATTTGTTGCTCTGATTCGTGATGATCTTTCGATTT 1495  
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1496 GACGAGCTATCTTGTGTTATTCCTTAATGAACAAATTAATCAACTTTGAAGACGT 1555  
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1556 CCCGTTGATGATTAATGATTAATGATTTCTTAAGCTGTCGAAATTTTGCAGCTGGCTTG 1615  
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1736 AAAGTCATCTTCTGTTCAAGTTCAATGAATGATTTGATCTTCAAAATATCTTTATAGCGT 1795  
658 AAAGTCATCTTCTGTTCAAGTTCAATGAATGATTTGATCTTCAAAATATCTTTATAGCGT 716  
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|  
|  
RESULT 3  
LOCUS CF304397 627 bp mRNA linear EST 15-AUG-2003  
DEFINITION ABF1--04-N21.g1 ABF3-overexpressing transgenic rice lamda phage

ACCESSION	CNDA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA clone ABF1--04-N21, mRNA sequence.
VERSION	CF304397
KEYWORDS	EST.
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group) Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE	1 (bases 1 to 627) Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
TITLE	Contact: Nahm B.H.
JOURNAL	Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myoungji University
COMMENT	Xongin, Kyeonggi, Korea Tel.: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr. location/Qualifiers
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SOURCE	1..627 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nackdong" /db_xref="taxon:39944" /clone="ABF1--04-N21" /risue_type="leaf" /dev_stage="14 days after germination" /lab_host="E.coli SOLR" /clone_lib="ABF1-overexpressing transgenic rice lambda phase cDNA library (ABF1)" /note="Vector: pBluescript SK(+); Site_1: EcoRI; site_2: XhoI; leaf was dried for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
ORIGIN	
Query Match	26.2%; Score 575; DB 6; Length 627;
Best Local Similarity	98.4%; Pred.No.1.le-117;
Matches 613; Conservative	0; Mismatches 5; Indels 5; Gaps 3;
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D	7 GGAAGACACCAAGACACGCGCATAGCAGAAAGCCGAGCGGCC-TCCTCGATCCATAT 65
D	1106 CTTCCGGTGCAGTCTTGSTGATCTCTCCCTCCACACTCCCTCCACAGGSTATGT 1165
D	66 CTTCCGGTGCAGTCTTGSTGATCTCTCCCTCCACACTCCCTCCACAGGSTATGT 125
D	1166 G---CCCTTCGGTCTCTTGATATTATTTAGTTGTAAGTACGGCGTGTGATGT 1222
D	126 GCCCTCCCTCGGTTCTTGAATTTATTTGTTCTAGGTTGTGTACGGCGTGTGATGT 185
D	1223 TAGAAAAGGGGATCTGTATCTGTAGTAGTTCCTGTTCTTGATTTGGANTAGAGGGGTTG 1282
D	186 TAGAAAAGGGGATCTGTATCTGTAGTAGTTCCTGTTCTTGATTTGGANTAGAGGGGTTG 245
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D	246 TTGATGTTGATGTTATTCGGTTCCGTTTGATTAAGTAGTATGTTCAATGTCGTGAGA 305
D	1343 GCCTATAGGAATGAATGTTTAGGGGTACGGAATCTTGCAATTTGTAGATCCTTTTG 1402
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D	366 TTTGAGGTAAATCAGACACCGGTGATTTTCTTGTTGTATATAAAGTACATTTGTTG 424

Oy	1463	GTCTCGAATTCGGTAGTGAAGGCTTCGCATTGACAAAGCATCCTTTGTTATTCCTT	1522
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Oy	1523	ATTGAACAAAATAATCCAACTTTGAAGACGGTCCCGTTGATGAGATTGAATGATT	1582
Dd	485	ATTGAACAAAATAATCCAACTTTGAAGACGGTCCCGTTGATGAGATTGAATGATT	544
Oy	1583	CTTAAGCTGTCCCAAAATTTGCGAGCTGGCTGTTTGATATACATGATCCCCATCAGGA	1642
Dd	545	CTTAAGCTGTCCCAAAATTTGCGAGCTGGCTGTTTGATATACATGATCCCCATCAGGA	604
Oy	1643	ATTGATGAAAAAGATTATATCC	1665
Dd	605	ATTGATGAAAAAGATTATATCC	627
RESULT 4			
CF306344		619 bp	mRNA linear EST 15-AUG-2003
LOCUS			
DEFINITION	HDA1--03-109.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDA1) Oryza sativa [japonica cultivar-group] cDNA clone HDA1--03-109, mRNA sequence.		
ACCESSION	CF306344		
VERSION	CF306344.1	GI:33678105	
KEYWORDS	EST.		
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Oryza sativa [japonica cultivar-group]		
REFERENCE	Bukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzaceae; Oryza.		
AUTHORS	Kim,J.S., Jun,K.W., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.		
TITLE	Large-scale Sequencing Analysis of Rice ESTs		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc./ Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahmbio.myongji.ac.kr.		
FEATURES			
SOURCE	Location/Qualifiers		
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	/db_xref="taxon:39947"		
	/clone="HDA1--03-109"		
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	/lab_host="E.coli SOLR"		
	/clone_1b="OSHDA1-overexpressing transgenic rice lambda phage cDNA library I (HDA1)"		
	/note="Vector: pBluescript SK(+). Site_1: EcoRI; Site_2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."		
ORIGIN			
Query Match	25.8%	Score 566.8;	DB 6; Length 619;
Best Local Similarity	98.1%;	Pred. No. 7.2e-116;	
Matches 606;	Conservative 0;	Mismatches 7;	Indels 5; Gaps 3;
Oy	1036	CCAAGAAGAGGAGGAGCACCAAGAGCACCGGACTATGACGAAGCGAGCGACCGCTCTT	1095
Dd	4	CGAGGAAGAGGAGGAGCACCAAGAGCACCGGACTATGACGAAGCGAGCGACCGC-TCTT	62
Oy	1096	CGATCCATATCTTCGGGTCCAGTTCCTTGTCGATCTCTTCCTCTCCACCTCCTCTCA	1155



Db		63	CGATCATATCTTCCGGTCGAGTTCTTGATGTGATCTCTTCCCTCCTCACCTCTCTCA	122
Oy		1156	CAGGGTAGTGC---CCCTTCGGTTGTCTTGATATTATTTGTTCTAAGTTTGTAACG	1212
Db		123	CAGGGTAGTGTGCTCCCTTCGGTTGTTCTTGAATTATTTGTTCTAAGTTTGTAACG	182
Oy		1213	GCGTTGATGTTAGAAAGGGAGTCTGTATCTGTGATGATTCCTGTTCTTGATTTGGGAT	1272
Db		183	GCCTTGATGTTAGAAAGGGAGTCTGTATCTGTGATGATTCCTGTTCTTGATTTGGGAT	242
Oy		1273	AGAGGGGTTCTTGATGTTGCATGTTATCGGTTCCGTTTGATTTAGTAGTATGGTTTTCAAT	1332
Db		243	AGAGGGGTTCTTGATGTTGCATGTTATCGGTTCCGTTTGATTTAGTAGTATGGTTTTCAAT	302
Oy		1333	CGTCTGAGAGCTCTATGSAATAATGATGTTTAGGGTAACGAATCTTCCGATTTTGTA	1392
Db		303	CGTCTGAGAGCTCTATGSAATAATGATGTTTAGGGTAACGAATCTTCCGATTTTGTA	362
Oy		1393	GTACCTTTGTTTGAAGTAAATCAGACACC GGATTTTGCTTGAGTAAATAAGTA	1452
Db		363	GTACCTTTGTTTGAAGTAAATCAGACACC GGATTTTGCTTGAGTAAATAAGTA	421
Oy		1453	CATTGTTGTTGCCCGATTCGAGTAGATGATGCTTCGATTTGACGAAGTATCTTTC	1512
Db		422	CATTGTTGTTGCCCGATTCGAGTAGATGATGCTTCGATTTGACGAAGTATCTTTC	481
Oy		1513	TTTATTCCTTATTTGAACAATAATTCGAATTTGAGAAGCGTCCGTTGATGAGATGA	1572
Db		482	TTTATTCCTTATTTGAACAATAATTCGAATTTGAGAAGCGTCCGTTGATGAGATGA	541
Oy		1573	ATGATGATTTCTTAAAGCTGTCCAAATTTTGGCAGCTGGCTTTAATACAGATGCC	1632
Db		542	ATGATGATTTCTTAAAGCTGTCCAAATTTTGGCAGCTGGCTTTAATACAGATGCC	601
Oy		1633	CCATCAGCAAAATTCATGA	1650
Db		602	CCATCAGCAAAATTCATGA	619
RESULT 5				
CKO38003				
LOCUS				
DEFINITION		CKO38003	585 bp mRNA linear EST 04-FEB-2005	
ACCESSION		41117Briccg_14440.y1	Oryza sativa cv. 93-11 tillering whole plant	
VERSION		CDNA library Oryza sativa cDNA 5', mRNA sequence.		
KEYWORDS		CKO38003		
SOURCE		CKO38003.1	GI:58609970	
ORGANISM		EST.		
AUTHORS		Oryza sativa		
REFERENCE		Oryza sativa		
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
		Ehharoidaeae; Oryzeae; Oryza.		
		1 (bases 1 to 585)		
TITLE		Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W.,		
JOURNAL		Hu,S., Zeng,C., Zhang,D., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X.,		
PUBMED		Zheng,H., Cong,L., Lin,L., Yin,J., Geng,J., Li,G., Shi,D., Liu,J.,		
COMMENT		Lv,H., Ren,J., Wang,J., Deng,Y., Ran,L., Shi,X., Wang,X., Wu,Q.,		
		Li,C., Lei,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z.,		
		Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P.,		
		Wu,S. and Liu,J.		
		The Genomes of Oryza sativa: A History of Duplications		
		PLoS Biol. 3 (2), e38 (2005)		
		15685292		
		Contact: Yan Zhou		
		Bioinformatics Department		
		Hangzhou Genomics Institute		
		No.51 Zhijiang Road, Hangzhou 310008, China		
		Tel.: 86-571-56805886		
		Fax: 86-571-56805884		
		Email: zhouyan@genomics.org.cn		
		Seq primer: M13 Forward		
		High quality sequence stop: 585		
		POLYA=NO.		

FEATURES	source	location/Qualifiers
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		/culivar="93-11"
		/db_xref="taxon:4530"
		/tissue_type="whole plant"
		/dev_stage="tillering"
		/clone_lib="Oryza sativa cv. 93-11 tillering whole plant cDNA library"
ORIGIN		
Query Match	24.2%; Score 511; DB 7; Length 585;	
Best Local Similarity	98.3%; Pred. No. 7.3e-109;	
Matches 569; Conservative	0; Mismatches 5; Indels 5; Gaps 3	
Oy	1035 GCCAAGAAGAGGAGAGAGCACCAGACACGCGACTGACAGAGCCGACGACCGCTTCT	109
Db	9 GCCAAGAAGAGGAGAGAGCACCAGACACGCGACTGACAGAGCCGACGACCGCTTCT	67
Oy	1095 TCGATCCATATCTTCCGATCGATTTCTTGATCTTTCCCTCTCACCCTCTCTC	115
Db	68 TCGATCCATATCTTCCGATCGATTTCTTGATCTTTCCCTCTCACCCTCTCTC	127
Oy	1155 ACAGGGATATG---CCCTTCGGTTCCTGATTTATGCTCAGGTGATGATG	121
Db	128 ACAGGGATATGCTCTCCCTCGATTTCTTGATTTATGCTCAGGTGATGATG	187
Oy	1212 GGCCTGATGTTAAGAAAGGAGATCTGATCTGATGATTTCTGATTTGGGA	127
Db	188 GGCCTGATGTTAAGAAAGGAGATCTGATCTGATGATTTCTGATTTGGGA	247
Oy	1272 TAGAGGGGTTCTGATGTTGATGTTATCGGTTGATTTAGTATGATGTTTCA	133
Db	248 TAGAGGGGTTCTGATGTTGATGTTATCGGTTGATTTAGTATGATGTTTCA	307
Oy	1332 TCGTCTGAGAGCTCTATGAAATGAAATGTTAGGTTAGGTTAGGATCTTGCAATTTG	139
Db	308 TCGTCTGAGAGCTCTATGAAATGAAATGTTAGGTTAGGATCTTGCAATTTG	367
Oy	1392 AGTACCTTTGTTGAGGTAATATCAGACACCGGTGATTTGCTGTTATTAAGT	145
Db	368 AGTACCTTTGTTGAGGTAATATCAGACACCGGTGATTTGCTGTTATTAAGT	426
Oy	1452 ACATTTGTTGGTCTCGATTTCTGATGATGCTTCTCGATTTGACGACGATCTCTT	151
Db	427 ACATTTGTTGGTCTCGATTTCTGATGATGCTTCTCGATTTGACGACGATCTCTT	486
Oy	1512 GTTATATCCCATTTGAACAATAATATTCACCTTTGAAGAGGTCCTGATGATG	157
Db	487 GTTATATCCCATTTGAACAATAATATTCACCTTTGAAGAGGTCCTGATGATG	546
Oy	1572 AATGATGATCTTAAGGCTGTCCAAAATTTCCGACGCTG 1610	
Db	547 AATGATGATCTTAAGGCTGTCCAAAATTTCCGACGCTG 585	
RESULT 6		
CE303311	578 bp mRNA linear EST 15-AUG-2003	
LOCUS	ABR1-01-016.g1 ABR1-overexpressing transgenic rice lambda phage	
DEFINITION	cDNA library (ABR1) Oryza sativa [japonica cultivar-group] cDNA	
clone ABR1-01-016, mRNA sequence.		
ACCESSION	CE303311	
VERSION	CE303311.1 GI:33675072	
KEYWORDS	EST.	
SOURCE	Oryza sativa (japonica cultivar-group)	
ORGANISM	Oryza sativa (japonica cultivar-group)	
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
	Eubryophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
	Ehharitoidae; Oryzaceae; Oryza.	
REFERENCE	1 (bases 1 to 578)	
AUTHORS	Kim,J.-S., Jun,K.-M., Cheong,P.-J., Kim,M.-J., Lee,T.-H., Shin,Y.-C.,	

TITLE  
JOURNAL  
COMMENT

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

Location/Qualifiers

1. 578

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39347"

/clone="ABP1-01-016"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli SOLR"

/clone\_lib="ABP1-overexpressing transgenic rice lambda  
phage cDNA library (ABP1)"

/note="Vector: pBluescript SK(+); Site\_1: EcoRI; Site\_2:  
XhoI; Leaf was dried for 2hrs. cDNA was inserted into  
lambda Uni-Zap XR vector at 5' end with EcoRI and 3' end  
with XhoI site. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

## ORIGIN

Query Match

24.0%; Score 526; DB 6; Length 578;

Best Local Similarity 98.3%; Pred. No. 9, 6e-107;

Matches 564; Conservative 0; Mismatches 5; Indels 5; Gaps 3;

## FEATURES

source

1. 775

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="genomic DNA"

/cultivar="japonica"

/cultivar="Nipponbare"

/db\_xref="taxon:39347"

/clone="nbe0045B22r"

/tissue\_type="leaf"

/lab\_host="E. coli DH10B"

/clone\_lib="CUGI Rice BAC Library (EcoRI)"

/note="Vector: pBACindigo; Site\_1: EcoRI; Site\_2: EcoRI;  
Rice is the most important food crop in the world. Half of  
the world population, especially those inhabiting highly  
populated areas of the humid tropics and subtropics, rely  
on rice as their primary source of carbohydrate.  
Monocotyledonous rice is a diploid plant (2n=24) with a  
haploid genome equivalent of 431 Mbp (Arumuganathan and  
Earle, 1991). The relatively small genome of rice, three  
times larger than that of Arabidopsis, makes it suitable  
for genomic studies. In order to facilitate positional  
cloning, physical mapping and genome sequencing of rice,  
we have constructed a BAC library from Oryza sativa,  
Nipponbare variety using EcoRI as the cloning enzyme. The  
library contains 55,296 clones with an average insert size  
of 121 kb providing approximately 15 haploid genome  
equivalents. The deep coverage allows the isolation a  
particular sequence with a probability of 99.9%. Three  
high density filters, each containing 18,432 clones  
(doubly spotted), represent the whole library for colony  
screening and can be requested from the Clemson University  
BAC/EST Resource Center (www.genome.clemson.edu)."

## ORIGIN

Query Match

21.9%; Score 479.8; DB 9; Length 775;

Best Local Similarity 90.2%; Pred. No. 2, 1e-96;

Matches 564; Conservative 0; Mismatches 39; Indels 22; Gaps 4;

RESULT 7  
AO871933/c

LOCUS

DEFINITION

AO871933 775 bp DNA linear GSS 03-NOV-1999  
nbe0045B22r CUGI Rice BAC Library (EcoRI) Oryza sativa (japonica  
cultivar-group) genomic clone nbe0045B22r, genomic survey  
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Wing, R.A. and Dean, R.A.  
A BAC End Sequencing Framework to Sequence the Rice Genome  
Unpublished (1998)  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Seq primer: GGAAACAGCTATGACCATG  
Class: BAC ends  
High quality sequence start: 170  
High quality sequence stop: 311.  
Location/Qualifiers

1. 775

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="genomic DNA"

/cultivar="japonica"

/cultivar="Nipponbare"

/db\_xref="taxon:39347"

/clone="nbe0045B22r"

/tissue\_type="leaf"

/lab\_host="E. coli DH10B"

/clone\_lib="CUGI Rice BAC Library (EcoRI)"

/note="Vector: pBACindigo; Site\_1: EcoRI; Site\_2: EcoRI;  
Rice is the most important food crop in the world. Half of  
the world population, especially those inhabiting highly  
populated areas of the humid tropics and subtropics, rely  
on rice as their primary source of carbohydrate.  
Monocotyledonous rice is a diploid plant (2n=24) with a  
haploid genome equivalent of 431 Mbp (Arumuganathan and  
Earle, 1991). The relatively small genome of rice, three  
times larger than that of Arabidopsis, makes it suitable  
for genomic studies. In order to facilitate positional  
cloning, physical mapping and genome sequencing of rice,  
we have constructed a BAC library from Oryza sativa,  
Nipponbare variety using EcoRI as the cloning enzyme. The  
library contains 55,296 clones with an average insert size  
of 121 kb providing approximately 15 haploid genome  
equivalents. The deep coverage allows the isolation a  
particular sequence with a probability of 99.9%. Three  
high density filters, each containing 18,432 clones  
(doubly spotted), represent the whole library for colony  
screening and can be requested from the Clemson University  
BAC/EST Resource Center (www.genome.clemson.edu)."

Db

1 AATCGAAGAGTTCTGACCGCTTTTCAGCTCTCACTAACAATATAGGAAGCTGTCT 60  
|||||  
689 AATGAAAAAGTTTCGACCGCTTTTCAGCTCTCACTAACAATATAGGAAGCTGTCT 630

Oy		61	AAATTTAAATGAGCCTTATATATGTAGCGGTGAATTACGAACATACTAAGAAGAAACT	120
Db		629	AAAAATTAATATGAGACTTATATATGTAGCGGTGAATTACGAACATACTAAGAAGAAACT	570
Oy		121	CATCCACCCTACTTTAGTGCGCAATCGGGCTTAAATTAAGAAAGATCGCTACACTAGTTTCGT	180
Db		569	CATCACCTACTTTAGTGCGCAATCGGGCTTAAATTAAGAAAGATCGCTACACTAGTTTCGT	510
Oy		181	TTTCTTGTATTAATTAAGTGGGAAAATGAATCATTTATTTGCTTAGAATATATAGTTGCATC	240
Db		509	TTTTCTTGTATTAATTAAGTGGGAAAATGAATCATTTATTTGCTTAGAATATATAGTTGCATC	450
Oy		241	TCTGTCAAGAGTTTAAATTTATTCGAGGTACGCAATTAATGTCAACAACCTCTTGAAATA	300
Db		449	TCTGTCAAGAGTTTAAATTTATTCGAGGTACGCAATTAATGTCAACAACCTCTTGAAATA	390
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Db		389	AAAAATCTTTCTAGCTGNACTCAATGGGTAAAGAGACATATTTTTTTTTTAAAAAAAAT	330
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Db		329	AGAAATGAAGATATTTCTGAAACGTATCGGCCAAGATTTAAACATATATATATATTTAT	270
Oy		421	AGTTGTGCACTTCGTTATATATGCGACAGTCATTAAAGACATGCTTACTCCA-TCTCAATTT	479
Db		269	AGTTGTGCACTTCGTTATATATGCGACAGTCATTAAAGACATGCTTACTCCATTCACAATTT	210
Oy		480	TTATTAGTAATTAAGACAATTTGACTTATTTTATTTATTTATTTCTTTTTCGATTAGATG	539
Db		209	TTATTAGTAATTAAGACAATTTGACTTATTTTATTTTATTTTCTTTTTCGATTAGATG	165
Oy		540	CAAGGTACTTACGACACACACTTTGTGCTCATGTGATGATGTGAGTGCACCTCTC-ATAC	598
Db		164	CAAGGTACTTACGACACACACTTTGTGCTCATGTGATGATGTGAGTGCACCTCTCAATAC	110
Oy		599	ACGTTCAACTACGACACACTCTTCCA	623
Db		109	CCGTTCAACTACGACACACTCTCTA	85
RESULT_8				
AGS71481	LOCUS			
DEFINITION		AGS71481	848 bp DNA linear GSS 03-NOV-2004	
ACCESSION			Oryza sativa (indica cultivar-group) genomic DNA, BAC end sequence.	
VERSION		AGS71481	BAC clone:X0245F03_R, genomic survey sequence.	
KEYWORDS		AGS71481.1	GI:55337716	
SOURCE		GSS:		
ORGANISM		Oryza sativa (indica cultivar-group)		
REFERENCE		Oryza sativa (indica cultivar-group)		
AUTHORS		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
TITLE		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
JOURNAL		Einhartoidaeae; Oryzaceae; Oryza.		
REFERENCE		1	Katagiri,S., Wu,J., Ito,Y., Karasawa,W., Shibata,M., Kanamori,H.,	
AUTHORS			Karayasee,Y., Namiki,N., Matsunoto,T. and Sasaki,T.	
TITLE			End Sequencing and Chromosomal in silico Mapping of BAC Clones	
JOURNAL			Derived from an indica Rice Cultivar, Kasalath	
REFERENCE			Breeding Science 54, 273-279 (2004)	
AUTHORS			2 (bases 1 to 848)	
TITLE			Sasaki,T., Matsunoto,T. and Wu,J.	
JOURNAL			Submitted (29-OCT-2004) Takui Sasaki, National Institute of	
REFERENCE			Agrobiological Sciences, Rice Genome Research Program, Kamondai	
AUTHORS			2-1-2, Tsukuba, Ibaraki, 305-8602, Japan	
TITLE			(E-mail:teasaki@nias.affrc.go.jp, URL:http://rpg.dna.affrc.go.jp/,	
JOURNAL			Tel:81-298-38-7441, Fax:81-298-38-7468)	
REFERENCE			The orientation of the sequence is from SP6 side of the BAC clone.	
AUTHORS			Location/Qualifiers	
TITLE			1..848	
JOURNAL			/organism="Oryza sativa (indica cultivar-group)" "	
REFERENCE			/mol_type="genomic DNA"	

ORIGIN	Query Match	13.7%	Score 300;	DB 10;	Length 848;
Best Local Similarity	90.9%	Pred. No. 3,7e-56;			
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OY	1113	TCGAGTCTTGGTGCATCTCTCCCTCCCTCCACCTCTCTCCACAGGATATGTC--CCC	1165		
DB	1	TCGAGTCTTGGTGCATCTCTCCCTCCCTCCACCTCTCTCCACAGGATATGTCGCCCTCC	60		
OY	1170	TTCCGTTGTTCTTGAGTTTATTTGTTCTTAAGTTGTGTAGTACGGCCGTTGATTAAGAAA	1225		
DB	61	TTCCGTTGTTCTTAATTTATTTGTTCTTAAGTTGTGTAGTACGGCCGTTGATTAAGAAA	120		
OY	1230	GGGAGCTGTATCTGTGATGATCTCTGTTCTTGATTTGGGATAGAGGGCTTCTGATGT	1285		
DB	121	GGGAGCTGTATCTGTGATGATCTCTGTTCTTGATTTGGGATAGAGGGCTTCTGATGT	180		
OY	1290	TGCATGTTATCGTTCCGTTGGTTGATTAGTAGTAGTGTTCAATCGTCTGAGAGCTCAT	1345		
DB	181	TGCATGTTATCGTTCCGTTGGTTGATTAGTAGTAGTGTTCAATCGTCTGAGAGCTCAT	240		
OY	1350	GGAAATGAATGCTTTAGGGTACGGAATCTTGCGATTTTGTGAGTACTTTTGTGAGG	1405		
DB	241	GGAAATGAATGCTTTAGGGTACGGAATCTTGCGATTTGAGATCACTTTGTTGTTGGG	300		
OY	1410	TAAATCAGAGCACCGGTGATTTTTCCTGCTGATATAAAGTACATTGTTGCTCTCG	1465		
DB	301	TAAATCAGAGCACCGGTGATTTTTCCTGCTGATATAAAGTACATTGTTGCTCTCTCA	360		
OY	1470	ATTC 1473			
DB	361	GTCC 364			
RESULT 9	CF305170	324 bp	mRNA	linear	EST 15-AUG-2003
LOCUS	ABP1--06-P15.g1	ABP3-overexpressing transgenic rice lambda phase			
DEFINITION	CDNA library (ABP1) Oryza sativa (japonica cultivar-group) cDNA				
ACCESSION	CF305170				
VERSION	CF305170.1	GI:33676931			
KEYWORDS	EST.				
SOURCE	Oryza sativa (japonica cultivar-group)				
ORGANISM	Oryza sativa (japonica cultivar-group)				
REFERENCE	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,I.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003) Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.				
TITLE	ABP1				
JOURNAL					
COMMENT					
FEATURES	Source				
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	/db_xref="taxon:39947"				
	/clone="ABP1--06-P15"				
	/rissue_type="leaf"				
	/dev_stage="14 days after germination"				

/lab\_host="E.coli SOLR"  
/clone.lib="ABF3-overexpressing transgenic rice lambda  
phage cDNA library (ABF1)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; Leaf was dried for 2hrs. cDNA was inserted into  
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end  
with XhoI site. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

## ORIGIN

Query Match 13.0%; Score 286.2; DB 6; Length 324;  
Best Local Similarity 97.8%; Pred. No. 4.1e-53;  
Matches 312; Conservative 0; Mismatches 3; Indels 4; Gaps 2;

1046 GGAGGACCAAGACAGCAGCAGCTAGCAGACCGGAGCGCCCTTCGATCCATAT 1105  
7 GGAGGACCAAGACAGCAGCAGCTAGCAGACCGGAGCGCCCTTCGATCCATAT 65  
1106 CTTCCGATCGAGTTCTTGATCGATCTCTCCCTCCACCTCTCTCAGAGGTATGT 1165  
66 CTTCCGATCGAGTTCTTGATCGATCTCTCCCTCCACCTCTCTCAGAGGTATGT 125  
1166 G---CCCTTCGATCGTTCTTGATTTATGTTCTAGGTTGTAGTACGGGCGTTGATGT 1222  
126 GCCTCCCTTCGATCGTTCTTGATTTATGTTCTAGGTTGTAGTACGGGCGTTGATGT 185  
1223 TAGGAAAGGGATCTGATCTGATGATGATCTCTCTCTGATTTGGGATAGAGGGGTTTC 1282  
186 TAGGAAAGGGATCTGATCTGATGATGATCTCTCTCTGATTTGGGATAGAGGGGTTTC 245  
1283 TTGATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1342  
246 TTGATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 305  
1343 GCTCTATGGAATGAATG 1361  
306 GCTCTATGGAATGAATG 324

RESULT 10 288 bp mRNA linear EST 15-AUG-2003  
LOCUS CF304743  
DEFINITION ABF1--05-N05-g1 ABF3-overexpressing transgenic rice lambda phage  
cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA  
clone ABF1--05-N05, mRNA sequence.  
ACCESSION CF304743  
VERSION CF304743.1 GI:33676504  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrharioideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 288)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
1. 288  
FEATURES  
source  
1. 288  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
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/lab\_host="E.coli SOLR"  
/clone.lib="ABF3-overexpressing transgenic rice lambda  
phage cDNA library (ABF1)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; Leaf was dried for 2hrs. cDNA was inserted into  
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end  
with XhoI site. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

## ORIGIN

Query Match 11.3%; Score 248.6; DB 6; Length 288;  
Best Local Similarity 97.2%; Pred. No. 1.1e-44;  
Matches 275; Conservative 0; Mismatches 4; Indels 4; Gaps 2;

1046 GGAGGACCAAGACAGCAGCAGCTAGCAGACCGGAGCGCCCTTCGATCCATAT 1105  
7 GGAGGACCAAGACAGCAGCAGCTAGCAGACCGGAGCGCCCTTCGATCCATAT 65  
1106 CTTCCGATCGAGTTCTTGATCGATCTCTCCCTCCACCTCTCTCAGAGGTATGT 1165  
66 CTTCCGATCGAGTTCTTGATCGATCTCTCCCTCCACCTCTCTCAGAGGTATGT 125  
1166 G---CCCTTCGATCGTTCTTGATTTATGTTCTAGGTTGTAGTACGGGCGTTGATGT 1222  
126 GCCTCCCTTCGATCGTTCTTGATTTATGTTCTAGGTTGTAGTACGGGCGTTGATGT 185  
1223 TAGGAAAGGGATCTGATCTGATGATGATCTCTCTCTGATTTGGGATAGAGGGGTTTC 1282  
186 TAGGAAAGGGATCTGATCTGATGATGATCTCTCTCTGATTTGGGATAGAGGGGTTTC 245  
1283 TTGATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1325  
246 TTGATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 288

RESULT 11 239 bp mRNA linear EST 05-FEB-2005  
LOCUS CK042297  
DEFINITION 43579riceh\_11650.y1 Oryza sativa cv. P646 panicle fertile cDNA  
library Oryza sativa (indica cultivar-group) cDNA 5', mRNA  
sequence.  
ACCESSION CK042297  
VERSION CK042297.1 GI:58653617  
KEYWORDS EST.  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrharioideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 239)  
AUTHORS Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W.,  
Hu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X.,  
Zheng,H., Cong,L., Lin,L., Yin,J., Geng,J., Li,G., Shi,J., Liu,J.,  
Lv,H., Li,J., Wang,J., Deng,Y., Ran,L., Shi,X., Wang,X., Wu,Q.,  
Li,C., Ren,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z.,  
Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P.,  
Wu,S. and Liu,J.  
TITLE The Genomes of Oryza sativa: A History of Duplications  
JOURNAL Plos Biol. 3 (2), e38 (2005)  
PUBMED 15685292  
COMMENT Contact: Yan Zhou  
Bioinformatics Department  
Hangzhou Genomics Institute  
No.51 Zhijiang Road, Hangzhou 310008, China  
Tel: 86-571-56805886  
Fax: 86-571-56805884  
Email: zhouyan@genomics.org.cn  
Seq primer: M13 Forward  
High quality sequence stop: 239  
POLYA=No.

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1. 239  
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ORIGIN

Query Match 9.3%; Score 204.2; DB 7; Length 239;  
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Matches 230; Conservative 0; Mismatches 3

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OY 1096 CGATCCATATCTTCCGATCGAGTTCTGGTCGATCTCTCCCTCCACCTCTCTCA 1155  
DB 63 CGATCCATATCTTCCGATCGAGTTCTGGTCGATCTCTCCCTCCACCTCTCTCA 122

OY 1156 CAGGATATGTC--CCCTTCGATGTTCTTGATTTATTTGTTCTAGTTGTGTGATCGG 1212  
DB 123 CAGGATATGTCCTCCCTTCGATGTTCTTGATTTATTTGTTCTAGTTGTGTGATCGG 182

OY 1213 GCGTGTAGTTTGAAGAAAGGAGATCTGATCTGTGATGATTCCTGTTCTTGATTTGG 1269  
DB 183 GCGTGTAGTTTGAAGAAAGGAGATCTGATCTGTGATGATTCCTGTTCTTGATTTGG 239

RESULT 12  
LOCUS CR291032 844 bp mRNA linear EST 27-FEB-2004  
DEFINITION CR291032 Oryza sativa library (Han B) Oryza sativa cDNA clone  
Y604h07p5, mRNA sequence.  
ACCESSION CR291032  
VERSION CR291032.1 GI:44677598  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 844)  
Han, B., Feng, Q., Huang, Y. C., Ying, K., Li, Y., Guan, J. P., Zhu, J. J.,  
Zhao, Q., Hu, X., Liu, Y. L., Wu, J., Yu, Z., Chen, L., Fan, D. L.,  
Weng, Q. J., Zhang, L., Lu, Y. Q., Yu, S. L., Liu, X. H., Lu, T. T.,  
Zhang, Y. J., Lu, Y., Li, C., Li, T., Zhang, Y., Hu, H., Jia, P. X.,  
Zhang, L., Lan, L. F., Chen, W., Wu, S. A. and Xue, Y. B.  
Rice cDNA EST clone  
Unpublished (2003)  
COMMENT  
TITLE JOURNAL  
JOURNAL  
COMMENT  
Contact: Han Bin  
National Center for Gene Research  
Chinese Academy of Sciences  
500# Cao Bao Road, Shanghai 200233, China  
Email: bhan@ncgr.ac.cn  
Clone request: bhan@ncgr.ac.cn  
This is rice cDNA est clone  
Web site: http://www.ncgr.ac.cn.  
Location/Qualifiers  
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ORIGIN

Query Match 9.2%; Score 201.8; DB 7; Length 844;

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Db	24	GAGGAGAGCAAGAAAAACAAGACATCTCTCTCCATCTTATTAATTCCTCCCTT	83			
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Db	84	TTCCCTCTCTATATATGAGAGCATTCGAAGCCAAAGAGGAGAGCAACGAGCAAGCG	143			
Qy	1067	ACTGACGAAGACCGAGCGACCGCTTCTTGATCCATATCTTCGGTGCAGTTCTTGCTC	1128			
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RESULT 13						
LOCUS	BX929024	982 bp	mRNA	linear	EST 03-FEB-2004	
DEFINITION	BX929024 Oryza sativa library (Han B) Oryza sativa cDNA clone					
ACCESSION	BX929024					
VERSION	BX929024.1	GI:41884193				
KEYWORDS	EST.					
SOURCE	Oryza sativa					
ORGANISM	Oryza sativa					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.					
AUTHORS	1 (bases 1 to 982)					
TITLE	Han,B., Feng,Q., Huang,Y.C., Ying,K., Li,Y., Guan,J.P., Zhu,J.J., Zhao,Q., Hu,X., Liu,Y.L., Mu,J., Yu,Z., Chen,L., Fan,D.L., Weng,Q.J., Zhang,L., Lu,Y.Q., Yu,S.L., Liu,X.H., Lu,T.T., Zhang,Y.D., Lu,Y., Li,C., Li,T., Zhang,Y., Hu,H., Jia,P.X., Zhang,L., Lan,L.F., Chen,W., Wu,S.A. and Xue,Y.B.					
JOURNAL	Rice cDNA EST clone					
COMMENT	Unpublished (2003)					
	Contact: Han Bin					
	National Center for Gene Research					
	Chinese Academy of Sciences					
	500# Cao Bao Road, Shanghai 200233, China					
	Email: bhan@ncgr.ac.cn					
	Clone requests: bhan@ncgr.ac.cn					
	This is rice cDNA est clone					
	Web site: http://www.ncgr.ac.cn.					
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Db 514 AAATTTC 520

Search completed: April 21, 2006, 17:58:03  
Job time : 7880 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 21, 2006, 08:53:39 ; Search time 413 Seconds  
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9447.331 Million cell updates/sec

Title: US-10-541-315-1

Perfect score: 2195  
Sequence: 1 aatccgaaagtcttcgcac.....cacttcaccgcaagttc 2195

Scoring table: IDENTITY NUC  
Gapop 10\_0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/prodata/1/ina/6B.COMB.seq: \*  
5: /cgn2\_6/prodata/1/ina/H.COMB.seq: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	867.2	39.5	898	3	US-10-012-070A-50 Sequence 50, Appl
2	56.8	2.6	7218	2	US-08-232-463-14 Sequence 14, Appl
3	55.2	2.5	612	3	US-09-902-540-1357 Sequence 1357, Ap
4	53.8	2.5	601	3	US-09-949-016-196365 Sequence 196365,
5	53.8	2.5	601	3	US-09-949-016-196366 Sequence 196366,
6	53.8	2.5	601	3	US-09-949-016-196367 Sequence 196367,
7	53.8	2.5	451924	3	US-09-949-016-12896 Sequence 12896, A
8	53.8	2.5	451925	3	US-09-949-016-17305 Sequence 17305, A
9	53.6	2.4	700	3	US-09-735-271-1038 Sequence 1038, Ap
10	53.6	2.4	1141	3	US-09-806-708B-22 Sequence 22, Appl
11	52.8	2.4	16573	3	US-09-949-016-14876 Sequence 14876, A
12	51.2	2.3	998	3	US-09-122-400B-5 Sequence 5, Appl1
13	51	2.3	95255	3	US-09-949-016-17067 Sequence 17067, A
14	50.2	2.3	50000	3	US-09-662-254B-24 Sequence 24, Appl
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16	49.8	2.3	601	3	US-09-949-016-37150 Sequence 37150, A
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18	49.8	2.3	601	3	US-09-949-016-145868 Sequence 145868,
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28	49	2.2	5526	3	US-08-907-146-21 Sequence 21, Appl
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36	48.2	2.2	601	3	US-09-949-016-164405 Sequence 146405,
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42	47.8	2.2	1341	3	US-09-830-230A-572 Sequence 572, App
43	47.6	2.2	1410	3	US-09-830-230A-571 Sequence 571, App
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ALIGNMENTS

RESULT 1					
US-10-012-070A-50					
; Sequence 50, Application US/10012070A					
; Patent No. 6867293					
; GENERAL INFORMATION:					
; APPLICANT: Hawkes, Timothy					
; APPLICANT: Warner, Simon					
; APPLICANT: Andrews, Christopher					
; APPLICANT: Bachoo, Savinder					
; APPLICANT: Pickertill, Andrew					
; TITLE OF INVENTION: Herbicide Resistant Plants					
; FILE REFERENCE: 50490/UST					
; CURRENT APPLICATION NUMBER: US/10/012,070A					
; CURRENT FILING DATE: 2001-10-29					
; PRIOR APPLICATION NUMBER: PCT/GB00/01573					
; PRIOR FILING DATE: 2000-04-20					
; NUMBER OF SEQ ID NOS: 57					
; SOFTWARE: Patentin Ver. 2.0					
; SEQ ID NO 50					
; LENGTH: 898					
; TYPE: DNA					
; ORGANISM: Oryza sp.					
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Matches 893; Conservative 0; Mismatches 3; Indels 4; Gaps 2;					
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US-08-232-463-14  
 1 Sequence 14, Application US/08232463  
 2 Patent No. 5670367  
 3 GENERAL INFORMATION:  
 4 APPLICANT: DORNER, F.  
 5 APPLICANT: SCHEIFLINGER, F.  
 6 APPLICANT: FALKNER, F. G.  
 7 TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
 8 NUMBER OF SEQUENCES: 52  
 9 CORRESPONDENCE ADDRESS:  
 10 ADDRESSEE: Foley & Lardner  
 11 STREET: 1800 Diagonal Road, Suite 500  
 12 CITY: Alexandria  
 13 STATE: VA  
 14 COUNTRY: USA  
 15 ZIP: 22313-0299  
 16 COMPUTER READABLE FORM:  
 17 MEDIUM TYPE: Floppy disk  
 18 COMPUTER: IBM PC compatible  
 19 OPERATING SYSTEM: PC-DOS/MS-DOS  
 20 SOFTWARE: Patentin Release #1.0, Version #1.25  
 21 CURRENT APPLICATION DATA:  
 22 APPLICATION NUMBER: US/08/232.463  
 23 FILING DATE:  
 24 CLASSIFICATION: 435  
 25 PRIOR APPLICATION DATA:  
 26 APPLICATION NUMBER: US/07/935.313  
 27 FILING DATE:  
 28 APPLICATION NUMBER: EP 91 114 300.6  
 29 FILING DATE: 26-AUG-1991

```

1 ATTORNEY/AGENT INFORMATION:
2 NAME: BENT, Stephen A.
3 REGISTRATION NUMBER: 29,768
4 REFERENCE/DOCKET NUMBER: 30472/114 IMM
5 TELECOMMUNICATION INFORMATION:
6 TELEPHONE: (703)836-9300
7 TELEFAX: (703)683-4109
8
9
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11
12
13 TELEX: 899149
14 INFORMATION FOR SEQ ID NO: 14:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 7218 base pairs
17 TYPE: nucleic acid
18 STRANDEDNESS: single
19 TOPOLOGY: linear
20 IMMEDIATE SOURCE:
21 CLONE: pTZgpc-F18
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Query Match 2.6%; Score 56.8; DB 2; Length 7218;  
Best Local Similarity 6.6%; Pred. No. 0.0011;  
Matches 28; Conservative 221; Mismatches 173; Indels 0; Gaps 0;

Qy	1680	TTCCCTGCTTCGCAATTTGCTTAGTCCCGAATTTTTCCTCAATATCTTAAAAAG	1739
Db	1069	YY	1128
Qy	1740	TCACCTTCGTGTCAGTTCAATGAATGATGCTACAAATATGCTTTATAGCCTTATC	1799
Db	1129	YYY	1188
Qy	1800	CTACCTGAGTTCAGTTATATAGTAATACCCCTATAGTTATAGTCAGAGAAAGAACTTATC	1859
Db	1189	YYY	1248
Qy	1860	CGATTTCGATCTCCATTTTAAATATATAGAAATGAAGCTGATAGATAGCAGTATTCATT	1919
Db	1249	YYY	1308
Qy	1920	TGGAATATTTTATATAGTCTTACCCCTCATATATCTGAGACTGAAATCTGGCAGT	1979
Db	1309	YYY	1366
Qy	1980	AACGTCCCTCAATTTGTTTCAAAATCACATCGATTATCTATCGATATCCTCTGTAT	2039
Db	1369	YYY	1428
Qy	2040	CTACCTGTAGAGTTTCTTTTGGTTATTTCTTGACTGCTTGATTAACAGAAAGAAATTTA	2099
Db	1429	YYYYYGTACCAATTCCTTATCTCTTAACTCTGACATAGATAGGTAAATTAACAGTGA	1488
Qy	2100	TG 2101	
Db	1489	TG 1490	

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RESULT 3
US-09-902-540-1357/c
: Sequence 1357, Application US/0902540
: Patent No. 6833447
:
: GENERAL INFORMATION:
:
: APPLICANT: Goldman, Barry S.
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Slater, Steven C.
: APPLICANT: Wiegand, Roger C.
:
: TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
:
: FILE REFERENCE: 38-10(15849)B
:
: CURRENT APPLICATION NUMBER: US/09/902,540
:
: CURRENT FILING DATE: 2001-07-10
:
: PRIOR APPLICATION NUMBER: 60/217,883
:
: PRIOR FILING DATE: 2000-07-10
:
: NUMBER OF SEQ ID NOS: 16825
:
: SEQ ID NO 1357
:
: LENGTH: 612

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/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 196367
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-196367
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Query Match      2.5%; Score 53.8; DB 3; Length 601;
Best Local Similarity 53.0%; Pred. No. 0.0026;
Matches 115; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
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Qy 319 AACTCAATGGTAAAGAGATATTTTAAAAAAGATGAGATATTCGA 378
Db 260 AATTAAATATATATATATATATATATATATATATATATATATATAT 201
Qy 379 ACGTATCGGCAAGATTTAAACATATATATATATATATATATATATAT 438
Db 200 ACATATATATATATATATATATATATATATATATATATATATATATAT 141
Qy 439 ATCGACGTCATTAAGACATGCTCTACTCCATCTCAATTTTATAGTAATTAAGAC 498
Db 140 AATTATATATATATATATATATATATATATATATATATATATATATATAT 81
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Qy 499 AATTGACTTATTTTATTTATTTATCTTTTCGATTA 535
Db 80 AATTAAATATATATATATATATATATATATATATATATATATATATATAT 44
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RESULT 7
US-09-949-016-12896/c
/ Sequence 12896, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12896
/ LENGTH: 451924
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-12896
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Query Match      2.5%; Score 53.8; DB 3; Length 451924;
Best Local Similarity 53.0%; Pred. No. 0.024;
Matches 115; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
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Qy 319 AACTCAATGGTAAAGAGATATTTTAAAAAAGATGAGATATTCGA 378
Db 140711 AATTAAATATATATATATATATATATATATATATATATATATATATATAT 140652
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Qy 379 ACGTATCGGCAAGATTTAAACATATATATATATATATATATATATATAT 438
Db 140651 ACATATATATATATATATATATATATATATATATATATATATATATAT 140592
Qy 439 ATCGACGTCATTAAGACATGCTCTACTCCATCTCAATTTTATAGTAATTAAGAC 498
Db 140591 AATTATATATATATATATATATATATATATATATATATATATATATATAT 140532
Qy 499 AATTGACTTATTTTATTTATTTATCTTTTCGATTA 535
Db 140531 AATTAAATATATATATATATATATATATATATATATATATATATATATAT 140495
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RESULT 8
US-09-949-016-17305/c
/ Sequence 17305, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 17305
/ LENGTH: 451925
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-17305
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Query Match      2.5%; Score 53.8; DB 3; Length 451925;
Best Local Similarity 53.0%; Pred. No. 0.024;
Matches 115; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
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Qy 319 AACTCAATGGTAAAGAGATATTTTAAAAAAGATGAGATATTCGA 378
Db 140711 AATTAAATATATATATATATATATATATATATATATATATATATATATAT 140652
Qy 379 ACGTATCGGCAAGATTTAAACATATATATATATATATATATATATATAT 438
Db 140651 ACATATATATATATATATATATATATATATATATATATATATATATAT 140592
Qy 439 ATCGACGTCATTAAGACATGCTCTACTCCATCTCAATTTTATAGTAATTAAGAC 498
Db 140591 AATTATATATATATATATATATATATATATATATATATATATATATATAT 140532
Qy 499 AATTGACTTATTTTATTTATTTATCTTTTCGATTA 535
Db 140531 AATTAAATATATATATATATATATATATATATATATATATATATATATAT 140495
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RESULT 9
US-09-735-271-1038
/ Sequence 1038, Application US/09735271
/ Patent No. 6869762
/ GENERAL INFORMATION:
/ APPLICANT: Daily, Mark J.
/ APPLICANT: Hudson, Thomas J.
/ APPLICANT: Lander, Eric S.
/ APPLICANT: Rieux, John
/ APPLICANT: Stilmovitch, Kathy
/ TITLE OF INVENTION: IBD-RELATED POLYMORPHISMS
/ FILE REFERENCE: 2825.1025-002
/ CURRENT APPLICATION NUMBER: US/09/735, 271
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; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/170,257
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/196,046
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 2058
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1038
; LENGTH: 700
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(700)
; OTHER INFORMATION: n = A,T,C or G
US-09-735-271-1038

Query Match
Best Local Similarity 45.8%; Score 53.6; DB 3; Length 700;
Matches 220; Conservative 0; Mismatches 259; Indels 1; Gaps 1;

QY 60 TAAATATAAGAGCCTTATATATGACGCTGATTAAGTAACTAGTAAAGAAAAC 119
DB 111 TATGTATATATATATATATATATATATATATATATATATATATATATATAT 170
QY 120 TCATCCACTACTTATAGTGCATCCGGCTAA-ATAAAAAGAGTGCCTACCTAGTTTC 178
DB 171 TATATATATATATATATATATATATATATATATATATATATATATATATAT 230
QY 179 GTTTCCTTAGTATTAAGTGGAAATGAATCATTTGCTTAGAATATACCTTCA 238
DB 231 ATATATATATATATATATATATATATATATATATATATATATATATATAT 290
QY 239 TCTCTGTCAGTAAATTAATGAGGAGCATAATGTCATCAACTCTCTGAA 298
DB 291 TATATATATATATATATATATATATATATATATATATATATATATATAT 350
QY 299 TAAAAAAATCTTCTAGCTGAATCAATGGTAAAGAGATATTTTTTAAAAAAA 358
DB 351 ATATATATATATATATATATATATATATATATATATATATATATATATAT 410
QY 359 ATGAAATGAGATATTCGAACTATCGCAAAAGATTAAACATATATATATAT 418
DB 411 ATATATATATATATATATATATATATATATATATATATATATATATATAT 470
QY 419 ATAGTTTGGCATCTTATATATCGCAGTCATTAAGACATGCTTACATCTCAAT 478
DB 471 ATATATATATATATATATATATATATATATATATATATATATATATATAT 530
QY 479 TTTATTTAGTATTAAGACATTAATTTTATTTTATTTTATTTTTCGTTAGAT 538
DB 531 TATATATATATATATATATATATATATATATATATATATATATATATATAT 590

RESULT 10
US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
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; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.T., L.a., and B.n. PAB1 promoters
US-09-806-708B-22

Query Match
Best Local Similarity 8.4%; Score 53.6; DB 3; Length 1141;
Matches 57; Conservative 290; Mismatches 330; Indels 1; Gaps 1;

QY 1474 TGTATGATGCTCTCGATTTGACGAAGCTATCTTTGTTATTCCTTATGAACAAA 1533
DB 79 WKGWYKKKKYBACNNTSBRHARWKDLYBMTMTKMGKTGRHRYWRBARBDYD 138
QY 1534 ATATATCAACCTTGAAGACGCTCCGTTGANGAGATTAATGATGATTTTAAGCTGT 1593
DB 139 HHVYTAANNAMWTTCMKDKDXTKRWKWKNNATATGMDDTKYHMMNNNGCBTVWY 198
QY 1594 CCAAAATTTCCGAGCTGCTGTTTATAGTATGATGATGATGATGATGATGATG 1653
DB 199 KTDRLMSBRMNYGMBWKNWSYDVTYYWVDDCKRKVRKRWVTRGRMRYVAMBTA 258
QY 1654 CAGTATATATCTCTCAGAAACAGGGGATTCCTGTCTTCCGATTTGCTTATGCCAGA 1713
DB 258 HRRYNNGTBMAARYMTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 318
QY 1714 TTTTTCCTCCAAATATCTTAAAAAGTCACTTCTGTTCACTGATCAATGATGCT 1773
DB 319 SCWANNCRAGDANKDKWKKWMSAAGVYNNNNNNNNNNNNNNNNNNNNNNNNNNNN 378
QY 1774 ACAATATATGCTTTTATATACCTTATCCTAGCTGATGATGATGATGATGATGAT 1833
DB 379 ANAAAYSRKWTBYRKTWNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 438
QY 1834 TAGTTAGTACAGAGAAAGTATTCCTGATTTCTGATCTCATTTTATATATGAAT 1893
DB 438 TQKQKMTYYKKKANNCKKRAMDHCTHNNNTWKKMTYNNNNNNNNNNNNNNNNNNNN 498
QY 1894 GAAGTATGATTAAGACATGATTTGATTTGATTTTATTTTATGCTTCAACCCCTCA 1953
DB 499 VYTWYMMWRBYAH-ANNNNNDYMKWCACTWYKVCBSKWMNNYAAWYTSWNSRYR 557
QY 1954 TTAATCTGAGCTGAAGTCTGCGATGAGTCTGCTCATATTTGTTTCAATTCACATG 2013
DB 558 WTKNNNSWRSPSTRSBRANNYARABHGYKNTBWBHSHTBHBRAAGAAHYWMBYB 617
QY 2014 ATTATCTATCATTTATCCCTTGTATCTAGCTGAGAGTTCTTTTGGTATTCCTTG 2073
DB 618 ACHCHKAWYKAKKTAGAGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 677
QY 2074 ACTGCTGATTAAGAAAGAAATTTATGAAGCTGATTCGGGATGATTAAGCTGCTGT 2133
DB 678 YKBAANNAYYHANNNWGCNNATIDTRTWKNNNNNNNNNNNNNNNNNNNNNNNNNN 737
QY 2134 CTTATGATTCATTTCTT 2151
DB 738 AAAAVYAAKCHWRMANKW 755

RESULT 11
US-09-949-016-14876
; Sequence 14876, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
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? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: FastSeq for Windows Version 4.0.0
? SEQ ID NO 14876
? LENGTH: 16573
? TYPE: DNA
? ORGANISM: Human
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)..(16573)
? OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14876

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Query Match	2.4%	Score 52.8;	DB 3;	Length 16573;
Best Local Similarity	46.2%;	Pred. No. 0.014;		
Matches 135;	Conservative 0;	Mismatches 157;	Indels 0;	Gaps 0;

[illegible]

```

RESULT 12
US-09-122-400B-5
Sequence 5, Application US/09122400B
Patent No. 6245974
GENERAL INFORMATION:
APPLICANT: Michalowski, Susan
APPLICANT: Spiker, Steven
TITLE OF INVENTION: MATRIX ATTACHMENT REGIONS
FILE REFERENCE: Michalowski and Spiker
CURRENT FILING DATE: US/09/122,400B
PRIORITY FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 60/066,118
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 998
TYPE: DNA
ORGANISM: Nicotiana glauca
US-09-122-400B-5

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Query Match	2.3%;	Score 51.2;	DB 3;	Length 998;
Best Local Similarity	48.6%;	Pred. No. 0.013;		
Matches 170; Conservative	0;	Mismatches 178;	Indels 2;	Gaps 1;

QY	180	TTTTTCCTAGTAATTAAGGGGAAATGAAATCATTAATGCTAGAAATATAGTTCACAT	239
Db	278	TATTTTTTTATATAAAATGGAATACTGAAATATATTTTACTATAAATATGAAAAACGA	337
QY	240	CTCTGCTATGGAAGTAAATATATTCGAGGTAGCATATATGTATCA--AACTCTTCTTA	297
Db	338	AAATATGTTTTTTTTCAGTTTTTACAAAAAACTATTTTTGAAAAAAATGAAAAATATTTT	397
QY	298	ATATAAAAAATCTTTCTAGCTGAACATCAATGGGTAAAGAGATATTTTTTTTTTAAAAAAA	357

Db	398	CTAAACCAAGT	TTTGTGTA	AAAACTG	AAAAAAGC	TGAAATCA	ATTTTCTAA	AGC	45	
Qy	358	AATAGATGA	AGATATTC	GAAAGT	ATCGGCA	AGATTAA	CAATATAT	ATAATTT	417	
Db	458	AATTTTAT	TTGTGTA	AATCTG	GA	AAAAAAGT	CACTAA	AAAACTG	AAAAATATTT	517
Qy	418	TATAGTTG	TCATTCG	TATATCG	CAAGTCA	TTAAG	GACATG	CTTACT	GCATCTCAAT	477
Db	518	TTTCTA	ATTTTTT	TACAA	AAAAAACTG	CTTTAAAA	AAAAAGTGA	AAAAATTTT	CTTAABACAAT	577
Qy	478	TTTTATTT	AGTATTTA	AGACAT	TGACTTA	TTTTTA	TATATTA	ATCTTT	527	
Db	578	ATTTTGT	AAAAA	CTAAAAA	AAAAAATAT	TTCTCT	TTTTTTC	AGTTTT	627	

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RESULT 13
US-09-949-016-17067
; Sequence 17067, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17067
; LENGTH: 95255
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(95255)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17067

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Query Match	2.3%	Score 51;	DB 3;	Length 95255;
Best Local Similarity	43.8%;	Pred. NO. 0.067;		
Matches 267;	Conservative	0;	Mismatches 340;	Indels 2;
				Gaps 1

[illegible]

```
QY 541 AAGTACTTACGACACACTTGTGCTCATGTCATGTGAGTGCACCTCTCATACAC 600
DB 42318 AATATATATATATATATATATATATATATATATATATATATATATATATAT 42377
QY 601 GTTCACTGCGACACATCTCCAAATATCACTGGCTATTATATACATTTAGTAGCAATA 660
DB 42378 ATATTATATATATATATATATATATATATATATATATATATATATATATATAT 42437
QY 661 TCTGAATTCAGACACTTCACATCACCAGACACTTTATATATATCTAAATACAAAA 720
DB 42438 TATTATATATAT--AATTATATATATATATATATATATATATATATATATATATAT 42495
QY 721 ATATATTTACAGATATGCAATGAAAGATGAAACGACTATTTAGTTTTCATACAA 780
DB 42496 ATATATTTACAGATATATATATACAAATATATATATATATATATATATATATATACAAA 42555
QY 781 AAAAAAAA 789
DB 42556 TATATATATA 42564

RESULT 14
US-09-662-254B-24/C
; Sequence 24, Application US/09662254B
; Patent No. 6933145
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Li, Yi
; APPLICANT: Bawden, Alison Louise
; TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
; FILE REFERENCE: UF-221C1X1
; CURRENT APPLICATION NUMBER: US/09/662,254B
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 09/086,651
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/224,479
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 50000
; TYPE: DNA
; ORGANISM: Amsacta moorei entomopoxvirus
US-09-662-254B-24

Query Match 2.3%; Score 50.2; DB 3; Length 50000;
Best Local Similarity 46.0%; Pred. No. 0.084;
Matches 169; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

QY 175 TTTCGTTTCTTCTAGTAATTAAGTGGAAATGAATTCATTTTGTGTTAGATATACGTT 234
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QY 235 CACATCTGTCATGAGTAAATTAATTTGAGGTACCAATATTCATCAAACTCTCT 294
DB 44021 TTTTTCATCATGAAGATTAATTAATTAACATTAATATATATATATATATATATAT 43962
QY 295 TGAATTAATTAATCTTTCTAGTGAACCTCAATGGGTAAAGAGATATTTTTPAAA 354
DB 43961 TAAATTAATTAATGATATATCTTTTAAATATATATATAGACAAATATAGTTTTCAT 43902
QY 355 AAAAAATGAATGAATATTCGAAGTATCGGCAAGTTTAAACATATTAATATATA 414
DB 43901 TGGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 43842
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DB 43841 AAAAAATGTTTATATTAATATGATATGAAATTAACATTAATTAATTAATTAATTAAT 43782
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DB 43781 ATATTATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 43722
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QY 535 AGATGCA 541
DB 43721 ACATTCA 43715

RESULT 15
US-09-949-016-30531/C
; Sequence 30531, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30531
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-30531

Query Match 2.3%; Score 49.8; DB 3; Length 601;
Best Local Similarity 46.0%; Pred. No. 0.024;
Matches 168; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

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QY 111 AAAAAAACTCACTCACTCTTGTAGTGGCAATCGGCTAATTAATTAATTAATTAATTAAT 170
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QY 171 CTAGTTCTGTTTCTTCTAGTAATTAAGTGGAAAAATGAATCATTTTGTGATATATA 230
DB 314 ATATTATATATATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 255
QY 231 CGTTCATCTCTGTCATGAAGTTAATTTATTCGAGTACCAATTTGTCATCAAACTC 290
DB 254 AATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 195
QY 291 TTCTGAATTAATTAATCTTTCTAGCTGAACCTAATGGGTAAAGAGATATTTT 350
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QY 411 ATPAT 415
DB 74 AATPAT 70

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GenCore version 5.1.7  
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Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
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8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_str:\*  
11: gb\_sy:\*  
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13: gb\_vl:\*  
14: gb\_hcg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2195	100.0	2195	6	CO876145
2	2141.4	97.6	3192	15	OSGOS2G
3	2139.2	97.5	3032	6	CO895917
4	2133.4	97.2	9361	6	BD251965
5	2133.4	97.2	10629	6	BD251966
6	2131.6	97.1	105692	14	AP003953
7	2131.6	97.1	110000	15	AP008213_206
8	2131.6	97.1	144741	15	AP004674
9	2128.4	97.0	14203	11	AF294979
10	2128.4	97.0	14230	11	AF294980
11	2115.2	96.4	2191	6	AF294980
12	867.2	39.5	898	6	AR643981
13	867.2	39.5	898	6	AX044095
14	867.2	39.5	898	6	AX044183
15	124.2	5.7	752	15	AK120697
16	108.2	4.9	744	15	AF094774
17	94.6	4.3	1275	15	AK105037
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C 21	85.8	3.9	172647	15	AC130732	AC130732 Oryza sat
C 22	84.6	3.9	110000	15	AP008209_328	Continuation (329
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C 25	79.8	3.6	110000	15	AP008213_289	Continuation (290
C 26	79.8	3.6	146856	15	AP004675	AP004675 Oryza sat
C 27	79.8	3.6	180015	15	AP005167	AP005167 Oryza sat
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C 37	70.6	3.2	171101	15	AC144740	AC144740 Oryza sat
C 38	69.6	3.2	110000	15	AP008208_196	Continuation (197
C 39	69.6	3.2	110000	15	AP008208_197	Continuation (198
C 40	69.6	3.2	145086	15	AP005798	AP005798 Oryza sat
C 41	69.6	3.2	149119	15	AP004156	AP004156 Oryza sat
C 42	69.4	3.2	110000	15	AP008217_054	Continuation (55 o
C 43	69.4	3.2	142241	15	AC123523	AC123523 Oryza sat
C 44	69.4	3.2	339485	15	AF172282	AF172282 Oryza sat
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#### ALIGNMENTS

RESULT 1	CO876145	2195 bp	DNA	linear	PAT 04-OCT-2004
LOCUS	CO876145				
DEFINITION	Sequence 1 from Patent WO2004065596.				
ACCESSION	CO876145				
VERSION	CO876145.1	GI:53789748			
KEYWORDS					
SOURCE					
ORGANISM	Oryza sativa				
	Oryza sativa				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
	Ehrhartoideae; Oryzaceae; Oryza.				
REFERENCE	1				
AUTHORS	Hatzfeld, Y. and Inze, D.				
TITLE	Regulatory sequence				
JOURNAL	Patent: WO 2004065596-A 1 05-AUG-2004;				
	CropDesign N.V. (BE)				
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Best Local Similarity	100.0%;	Pred. No. 0;			
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QY	1	AATCGAAGAGTTCTGACCGTTTCAAGCTCTAACAATATAGGAAGTGTCT	60		
DB	1	AATCGAAGAGTTCTGACCGTTTCAAGCTCTAACAATATAGGAAGTGTCT	60		
QY	61	AAATATAAATGAGACTTATATATGAGCGCTGATTAAGTAAGTAAGAAACT	120		
DB	61	AAATATAAATGAGACTTATATATGAGCGCTGATTAAGTAAGTAAGAAACT	120		
QY	121	CATCACCCTACTTATGTCGCAATCGGCGCTAAATATAAAGAGTCCCTACAGTGTCT	180		
DB	121	CATCACCCTACTTATGTCGCAATCGGCGCTAAATATAAAGAGTCCCTACAGTGTCT	180		
QY	181	TTTCCTAGTATTAATGAGTAATGAAATGAAATCATATTGCTTAGAATATACCTTCATC	240		
DB	181	TTTCCTAGTATTAATGAGTAATGAAATGAAATCATATTGCTTAGAATATACCTTCATC	240		

Db 181 TTTCCCTAGTAAATTAAGTGGGAAAATGAATCATTAATTCCTTAAGATATACCTTCACATC 240  
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 Db 241 TCTGTCAGTAAGTAAATTAATTCGAGGTAGCCATATTCGATCCAACTCTCTGGAATA 300  
 Qy 301 AAAAAATCTTCTAGCTGAATCTCAATGGGTAAAGAGATATTTTCTTAAAAAANAAT 360  
 Db 301 AAAAAATCTTCTAGCTGAATCTCAATGGGTAAAGAGATATTTTCTTAAAAAANAAT 360  
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 Db 421 AGTTTGTCATTCGTTATATCGCAGTCAATTAAGGACATGTCATCTCAATCTCAATTTT 480  
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 Db 661 TCTGAATTCAGACACTTCAACATCAACAGACCACTTTTAAATATATCTTAAAAATACAAAA 720  
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 Db 781 AAAAAAAGATTTTGGCTGTCGCGGAGGCGCAATCTCCCAATTTGGGACACAGGCA 840  
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 Db 841 CAACAGAGTGTGCGCCACAGAACCAACCAAAAAACGATATCTAACGAGAGACAGCA 900  
 Qy 901 AGTCCGCAACACTTTTAAACAGAGGCTTTGGCGCAGAGAGAGAGAGAGAGAGAGAG 960  
 Db 901 AGTCCGCAACACTTTTAAACAGAGGCTTTGGCGCAGAGAGAGAGAGAGAGAGAGAG 960  
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RESULT 2  
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 ACCESSION X51910.1 GI:20237  
 VERSION GOS2 gene; rice.  
 KEYWORDS Oryza sativa (indica cultivar-group)  
 SOURCE Oryza sativa (indica cultivar-group)  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;



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 DEFINITION Sequence 7 from Patent WO2004090142.  
 ACCESSION CO895917  
 VERSION CO895917.1 GI:55467905  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 synthetic construct  
 synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE  
 AUTHORS Sanz Molinero, A.I.  
 TITLE Plants having modified growth characteristics and method for making the same  
 JOURNAL Patent: WO 2004090142-A 7 21-OCT-2004; CropDesign N.V. (BE)  
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 Qy 421 AGTTTGACATTTGTTATATGACGATTAATGAGACATGCTTAACTACATCTCAATTTT 480  
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Qy	1329	CAATCGTCGAGAGACCTCTATGAAATGAAATGTTTAAAGGTACGAAATCTTTCGATTTT	1388
Db	6405	CAATCGTCGAGAGACCTCTATGAAATGAAATGTTTAAAGGTACGAAATCTTTCGATTTT	6346
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Db	6345	GTGAGTACCTTTTGTGTTGAGGTAAATCAGAGCACCGGTGATTTTGTGTTGATTAATA	6286
Qy	1449	AGTACATTGTTGGTCCGATTCCTGATGAGTATGCTTCTCGATTTGACGAAGCTATCC	1508
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Qy	1509	TTTGTATTATCCCTATATGAAACAAAATAATCCAACTTTGAAGACGGTCCGTTGATGAGA	1568
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Qy	1569	TTGAATGATGATTCTTTAAGCTGTGCCAAAATTTGGCAGCTGGCTGTTTATATACATA	1628
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Qy	2109	AATCGGATATGTTATATATGCTGTTGTTCTTATGATTCATTTTCTTTTGCAAGTTCTTGCT	2168
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LOCUS	AP003953	105692 bp	DNA linear HTG 21-MAR-2002
DEFINITION	Oryza sativa (japonica cultivar-group) chromosome 7 clone		
ACCESSION	U01365.D04.*** SEQUENCING IN PROGRESS ***.		
VERSION	AP003953.1 GI:15021923		
KEYWORDS	HTG, HTGS, PHASE2.		
SOURCE	Oryza sativa (japonica cultivar-group)		

ORGANISM	Oryza sativa (Japanese cultivar-group) Eukaryote; Viridiplantae; streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.				
REFERENCE	1 Sasaki, T., Matsumoto, T. and Yamamoto, K. Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC clone:OU1365 D04				
JOURNAL	2 (bases 1 to 105692) Published only in Database (2001)				
AUTHORS	Sasaki, T., Matsumoto, T. and Yamamoto, K.				
TITLE	Direct Submission				
COMMENT	Submitted (25-JUL-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program, Kamondal 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail: sasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/, Tel: 81-298-38-7441, Fax: 81-298-38-7468) The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data. NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved. * NOTE: This is a 'working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved.				
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DB	22907	AAATCGAAAAGTTTCGCAACCGTTTTCACGTCCTAATCAATATAGGAAACGTCGT	22848		
OY	61	AAATATAAATGAGACCTTATATGAGGCGTATACATGAACTATAGAAAACCT	120		
DB	22847	AAATATAAATGAGACCTTATATGAGGCGTATACATGAACTATAGAAAACCT	22768		
OY	121	CATCACTCACTTATGATGCGAATCGGCGTAAATAAAAAAGTCGCTACATGATTTGCT	180		
DB	22787	CATCACTCACTTATGATGCGAATCGGCGTAAATAAAAAAGTCGCTACATGATTTGCT	22728		
OY	181	TTTCTCTTAGATTAATAGTGGAAAATGAATCATTTTCTTAGATATACGTTCAATC	240		
DB	22727	TTTCTCTTAGATTAATAGTGGAAAATGAATCATTTTCTTAGATATACGTTCAATC	22668		
OY	241	TCGTCATGAAGTTAAATTTATGAGAGTACCATTAATGTCATCAAACTCTTCTGAATA	300		
DB	22667	TCGTCATGAAGTTAAATTTATGAGAGTACCATTAATGTCATCAAACTCTTCTGAATA	22608		
OY	301	AAAAAATCTTCTAGCTGAACCTCAATGCGTAAAGAGATATTTTTTTTAAAAAAAAT	360		
DB	22607	AAAAAATCTTCTAGCTGAACCTCAATGCGTAAAGAGATATTTTTTTTAAAAAAAAT	22548		
OY	361	AGAAATGAAGTATTTCTGAACGATTCGCAAAAGTTTAAACATATATATATTTAT	420		
DB	22547	AGAAATGAAGTATTTCTGAACGATTCGCAAAAGTTTAAACATATATATATTTAT	22488		
OY	421	AGTTTGCAATGCTTATATGAGAGCTATTAAGCATGATGCTTACATGCAATTTT	480		



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Query Match 97.1%; Score 2131.6; DB 15; Length 110000;

Best Local Similarity 99.3%; Pred. No. 0;

Matches 2183; Conservative 0; Mismatches 9; Indels 6; Gaps 4;

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RESULT 8  
AP004674/c

LOCUS AP004674 144741 bp DNA linear PLN 22-JUL-2004

DEFINITION Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 7,  
PAC clone:P0681F05.

ACCESSION AP004674

VERSION AP004674.2 GI:26017274

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Euhartoidaeae; Oryzeae; Oryza.

REFERENCE

1 Sasaki, T., Matsumoto, T. and Yamamoto, K.  
Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC  
clone:P0681F05  
Published Only in Database (2002)

JOURNAL TITLE

2 (bases 1 to 144741)

REFERENCE AUTHORS

Sasaki, T., Matsumoto, T. and Yamamoto, K.

TITLE Direct Submission

JOURNAL

Submitted (23-JUN-2002) Takui Sasaki, National Institute of  
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2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
(E-mail:sasakit@nias.affrc.go.jp, URL:http://rsg.dna.affrc.go.jp/,  
Tel:+81-298-38-7441, Fax:+81-298-38-7468)

COMMENT

On Dec 3, 2002 this sequence version replaced gi:19307752.  
Genes were predicted from the integrated results of the following:  
GENSCAN (<http://CCR-061.mt.edu/GENSCAN.html>), FGENESH  
[\(http://www.softberry.com/\)](http://www.softberry.com/), GeneMark.hmm  
[\(http://opal.biology.gatech.edu/GeneMark/\)](http://opal.biology.gatech.edu/GeneMark/), GlimmerX  
[http://www.tigr.org/tcb/glimmerx/glmr\\_form.html](http://www.tigr.org/tcb/glimmerx/glmr_form.html), RICEHMM  
[\(http://rsg.dna.affrc.go.jp/RiceHMM/\)](http://rsg.dna.affrc.go.jp/RiceHMM/), SplicePredictor  
<http://bioinformatics.iastate.edu/cgi-bin/sp.cgi>, slm4  
<http://globin.cse.psu.edu/html/docs/slrm4.html>, gap2  
[\(http://www.tigr.org/software/glimmer/\)](http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The

genomic sequence was searched against NCBI NonRedundant Protein database, nr (<ftp://ncbi.nlm.nih.gov/blast/db>) and the cDNA sequence database at RGP or DDBJ. NonRedundant Protein database regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. A gene with identity or significant DDBJ homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.

The orientation of the sequence is from 5' to 3' of the cDNA clone. This sequence of P0681F05 clone has an overlap with OSJNB0007H12 (DDBJ: AP004990) clone at 5' end and with OSJNB004C15 (DDBJ: AP005850) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://xsp.dna.affrc.go.jp/GenomeSeq.html>.

Location/Qualifiers

1..144741

organism="Oryza sativa (japonica cultivar-group)"

mol\_type="genomic DNA"

cultivar="Nipponbare"

db\_xref="taxon:39947"

chromosome="7"

clone="P0681F05"

3263..3469

gene="P0681F05.101"

<3263..>3469

note="P0681F05.101"

note="start and end point are not identified"

3263..3469

gene="P0681F05.101"

note="similar to Oryza sativa chromosome 7, OJ1656.E1.24"

codon\_start=1

product="hypothetical protein"

protein\_id="BAC45137.1"

db\_xref="GI:27261021"

translation="MADGYRRLVTLTAATLVPAACTSSAGAGMOCVPAARCGRLFGVA TGGDRORCGMPKRAVESAFOMAD"

complement(6526..7985)

gene="P0681F05.102"

complement(join(6526..6561,6842..6925,7110..7217,7735..7831,7975..>7985))

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note="start and end point are not identified"

complement(join(6526..6561,6842..6925,7110..7217,7735..7831,7975..7985))

gene="P0681F05.102"

note="predicted by FGENESH etc."

codon\_start=1

product="hypothetical protein"

protein\_id="BAC45138.1"

db\_xref="GI:27261022"

translation="MTIKRPMSLHQSMDPDSAGFAGANDVNCCEFTSRRYIAEK SRAPAPSSSHGLASAPCEMSPCKMKQSPVLI FMPKPKDRGTRYIGSNPLGMEQV MRPTRFMS"

complement(13012..13446)

gene="P0681F05.103"

complement(join(13012..13105,13319..>13446))

gene="P0681F05.103"

note="start and end point are not identified"

complement(join(13012..13105,13319..13446))

gene="P0681F05.103"

note="predicted by GeneMark.hmm etc."



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CDS  
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gene  
mRNA  
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CDS  
CDS  
mRNA  
CDS

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CDS  
pseudogene, transposase"  
pseudo  
19824..20405  
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23751..25240  
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AALFTSTWSRLARPVYKLFNAVAEDLIVKGRGVGVYTNMALVSMNHDSQMDP  
NWESRVVSSCGHDPFGATGVKRLQDIDMIDAVPGRALDMNTABDEIVRLTRVY  
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/note="hypothetical ORF  
predicted by GENSCAN

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mRNA  
misc\_feature  
gene  
mRNA  
gene  
mRNA  
Query Match  
Best local Similarity 99.3%; Pred. No. 0;  
Matches 2183; Conservative 0; Mismatches 9; Indels 6; Gaps 4;

this category is not included in INRSP standard"  
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probably inactive due to including stop codon(s) in CDS"  
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join(28697..28907,28986..29086,29178..29380,29774..30188)  
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35460 AATCCGAAAGTTTGTGACCGTTTTCAGCTCTTAACAATATAGGAACTGTGCT 35401  
61 AATATTAATGACCTTATATATATAGCGCTGATACCTATATGTAAGAAAACT 120  
35400 AATATTAATGACCTTATATATATAGCGCTGATACCTATATGTAAGAAAACT 35341  
121 CATCCACCTATTGTGCAATCGGGCTAAATTAAGAGAGCGTACCTAGTTTGGT 180  
35340 CATCCACCTATTGTGCAATCGGGCTAAATTAAGAGAGCGTACCTAGTTTGGT 35281  
181 TTTCCTAGTAATTAAGTGGAAATGAATCATTTATGCTTAAGATATACGTTCAATC 240  
35280 TTTCCTAGTAATTAAGTGGAAATGAATCATTTATGCTTAAGATATACGTTCAATC 35221  
241 TCTGTCATGAATTAATTTATGAGAGTATGCTATATGCTCAATCTCTTGAATA 300  
35220 TCTGTCATGAATTAATTTATGAGAGTATGCTATATGCTCAATCTCTTGAATA 35161  
301 AAAAAATCTTCTAGCTGAATCAATGGTAAAGAGATTTTTTTTTTAAAAAAAT 360  
35160 AAAAAATCTTCTAGCTGAATCAATGGTAAAGAGATTTTTTTTTTAAAAAAAT 35101  
361 AGAATGAGATATTTGAAAGTATCGGCAAAATTTAAACATATATATATTTAT 420  
35100 AGAATGAGATATTTGAAAGTATCGGCAAAATTTAAACATATATATATTTAT 35041  
421 AGTTGTGATTCGTTATATGCAAGCTCAATTAAGACATGCTTCACTCAATTTT 480  
35040 AGTTGTGATTCGTTATATGCAAGCTCAATTAAGACATGCTTCACTCAATTTT 34981  
481 TATTTAGTAATTAAGACATGCTTATTTTATATATCTTTTTCGATTGAGATG 540  
34980 TATTTAGTAATTAAGACATGCTTATTTTATATATCTTTTTCGATTGAGATG 34921  
541 AAGGTACTACGACACATTTGTGCTCATGTCATGTCATGTCATGTCATGTCAT 599  
34920 AAGGTACTACGACACATTTGTGCTCATGTCATGTCATGTCATGTCATGTCAT 34861  
600 CGTTCACTAGGACACATCTCAATATGCTCGCTATTTAATCAATTTAGATCAAT 659  
34860 CGTTCACTAGGACACATCTCAATATGCTCGCTATTTAATCAATTTAGATCAAT 34801  
660 ATCTGAATTCAGCACTTACCATCACCAGACACCTTTAATTAATCTTAATCAAAA 719  
34800 ATCTGAATTCAGCACTTACCATCACCAGACACCTTTAATTAATCTTAATCAAAA 34741

OY	720	ATAATTTTACAGAAATGCAATGAAAGATATGAAACGAATATATAGATTTCACATACA	779
Db	34740	ATAATATTTTACAGAAATGCAATGAAAGATATGAAACGAATATATAGATTTCACATACA	34681
OY	780	AAAAAAAAAAGAAATTTTGCTCTGTGCGGAGCGCCAAATCTCCATATTGGGACACAGGCA	839
Db	34680	AAAAAAAAAAGAAATTTTGCTGTGTGCGGAGCGCCAAATCTCCATATTGGGACACAGGCA	346211
OY	840	ACAAACAGATGCGCTGCCACACGAACCAACCAAAAAAGATATCTTAACGAGGACACGC	899
Db	34620	ACAAACAGATGCGCTGCCACACGAACCAACCAAAAAAGATATCTTAACGAGGACACGC	34561
OY	900	AAGTCGGCAACAATCTTTTAAACAGCAGGCTTTGGCGCAGAGAGAGAGAGAGGCAAA	959
Db	34560	AAGTCGGCAACAATCTTTTAAACAGCAGGCTTTGGCGCAGAGAGAGAGAGAGGCAAA	34501
OY	960	GAAACCAAGACATCTCTCTCTCCATCTATAAATTCCTCCCTCTTTCCTCTCTAT	1019
Db	34500	GAAACCAAGACATCTCTCTCTCTCTCCATCTATAAATTCCTCCCTCTTTCCTCTCTAT	344411
OY	1020	ATAGAGGCGATCCAGCCAAAGAGAGGAGAGACCAAGACACGCGACTAGACAGAGCC	1079
Db	34440	ATAGAGGCGATCCAGCCAAAGAGAGGAGAGACCAAGACACGCGACTAGACAGAGCC	34381
OY	1080	GAGGACCGGCTTCTTGATCCAAATCTTCGGTCGAGTCTTGCGATCTCTCCCTCCGC	1139
Db	34380	GAGGACCGGCTTCTTGATCCAAATCTTCGGTCGAGTCTTGCGATCTCTCCCTCCGC	34322
OY	1140	CTCCACCTCTCTCTCACAGGAGATGTC---CCCTCGGTGTCTTGAGTTTATGTTCT	1196
Db	34321	CTCCACCTCTCTCTCACAGGAGATGTC---CCCTCGGTGTCTTGAGTTTATGTTCT	34262
OY	1197	AGTGTGTAGTACGGCGTTGATGTTAGAAAGGGAGTCTGATCTGTGATGATTCCTG	1256
Db	34261	AGTGTGTGTAGTACGGCGCTTGATGTTAGAAAGGGAGTCTGATCTGTGATGATTCCTG	34202
OY	1257	TTCTTGATTTGGGATAGAGGGGCTTGAGATGTGATGCTATCGGTCGGTTGATTAAG	1316
Db	34201	TTCTTGATTTGGGATAGAGGGGCTTGAGATGTGATGCTATCGGTCGGTTGATTAAG	34142
OY	1317	TAGATGAGTTTCAATGCTGTGAGAGACTCTATGSAATGSAATGTTTAGGATACGAA	1376
Db	34141	TAGATGAGTTTCAATGCTGTGTGAGAGCTCTATGSAATGSAATGTTTAGGATACGAA	34082
OY	1377	TCTTGCAATTTGTGAGTACCTTTGTTGAGGTAAATCAGAGCACGGTGAATTTGCT	1436
Db	34081	TCTTGCAATTTGTGAGTACCTTTGTTGAGGTAAATCAGAGCACGGTGAATTTGCT	34022
OY	1437	TGTGTATATAAAGTACATTTGTTTGGTCTCGAATCTGTAGTGAATGCTTCGATTTG	1496
Db	34021	TGTGTATAT--AAATGATATTTGTTTGGTCTCGAATCTGTAGTGAATGCTTCGATTTG	33963
OY	1497	ACGAAGCATCTCTGTTTATATCCCTATTGAAACAAAAATATCAACTTTGAAAGCGTC	1556
Db	33962	ACGAAGCATCTCTGTTTATATCCCTATTGAAACAAAAATATCAACTTTGAAAGCGTC	33903
OY	1557	CCGTTGATGAGATTTGAATGATTTGATCTTAAAGCTGTCCAAAATTTGCGAGCTGCTGT	1616
Db	33902	CCGTTGATGAGATTTGAATGATTTGATCTTAAAGCTGTCCAAAATTTGCGAGCTGCTGT	33843
OY	1617	TTAATATACAGTAGTCCCAATCAAGAAATTCATGAAAAAGATTATATCTCAGAGAACAG	1676
Db	33842	TTAATATACAGTAGTCCCAATCAAGAAATTCATGAAAAAGATTATATCTCAGAGAACAG	33783
OY	1677	GGATTCCTGTCTCTCGAATTTGGTTAGTCCAGAAATTTTTCCTCCAAATATCTTAA	1736
Db	33782	GGATTCCTGTCTCTCGAATTTGGTTAGTCCAGAAATTTTTCCTCCAAATATCTTAA	33723
OY	1737	AAGTACATTTCTGTGTCAATGATGATGATGCTTACAAATATGCTTTATAGCGTT	1796
Db	33722	AAGTACATTTCTGTGTCAATGATGATGATGCTTACAAATATGCTTTATAGCGTT	33663
OY	1797	ATCTTAGCTGATTCAGTTTATAGTAAATACCCCTATAGTTTAGTACAGAGAAAGACTT	1856

Db	33662	ATCTTACTGTAGTTCAGTTTATATAGTATATACCCCTATAGTTTAGTCAGGAGAAAGAACTT	3360		
Oy	1857	ATCCGATTTCTGATCTCCATTTTAAATTATATATGAAATGAACCTGTAGATATAGCAGATATTC	1916		
Db	33602	ATCCGATTTCTGATCTCCATTTTAAATTATATGAAATGAACCTGTAGATATAGCAGATATTC	3354		
Oy	1917	ATTGGATTTATTTTTTTTATATAGCTTCACCCCTTCATTAATTCGAGCTGAAAGTCTGGC	1976		
Db	33542	ATTGGATTTATTTTTTTTATATAGCTTCACCCCTTCATTAATTCGAGCTGAAAGTCTGGC	3348		
Oy	1977	ATGAAGCTGCTCAATTTTGTTCGAAATTCACATCGATTATCTATGATTAATCTCTTG	2036		
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Db	33422	TATCTACCTGTAGAGTTTCTTTTGGTTATTCCTTGACTGCTTGATTACAGAAAGAAAT	3336		
Oy	2097	TTATGAAGCTGTATCGGAGATGATATACGCTTGCTTATATATCATTCATTCCTTTGTGC	2156		
Db	33362	TTATGAAGCTGTATCGGAGATGATATACGCTTGCTTATATATCATTCATTCCTTTGTGC	3330		
Oy	2157	AGTCTTGATGTAGCTTGCACATTCACAGCAAGATT	2194		
Db	33302	AGTCTTGATGTAGCTTGCACATTCACAGCAAGATT	33265		
RESULT 9	AF294979	14203 bp	DNA	circular	SYN 24-MAY-2002
LOCUS	AF294979				
DEFINITION	Binary vector pINDEK1, complete sequence.				
ACCESSION	AF294979				
VERSION	AF294979.1	GI:11559663			
KEYWORDS	Binary vector pINDEK1				
SOURCE	Binary vector pINDEK1				
ORGANISM	other sequences; artificial sequences; vectors.				
REFERENCE	1 (bases 1 to 14203)				
AUTHORS	Ouwertkerk, P. B., de Kam, R. J., Hoge, V. H. and Meijer, A. H.				
TITLE	Glucocorticoid-inducible gene expression in rice				
JOURNAL	Planta 213 (3), 370-378 (2001)				
PUBMED	11506359				
REFERENCE	2 (bases 1 to 14203)				
AUTHORS	Ouwertkerk, P. B. P.				
TITLE	Direct Submision				
JOURNAL	Submitted (11-AUG-2000) Dept. of Molecular Cell Biology, Institute for Molecular Plant Sciences, Wassenaarseweg 64, Leiden 2333 AL, Netherlands				
COMMENT	pINDEK1 is a binary vector designed for glucocorticoid-inducible gene expression in plants and is optimized for use in rice; pINDEK1 is part of a series of four pINDEK vectors (Genbank Accession Numbers AF294979-AF294982). pINDEK vectors are based on parts of pCM8B1A-1300 encoded by Genbank Accession Number AF234296 and pTR7002 (Aoyama, T. and Chua N.-H., 1997, Plant J. 11:605-612).				
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5'UTR	1058..1194				
exon	/number=1				
intron	1195..2157				
	/note="derived from Goss2"				
	/number=1				
exon	2158..3552				
	/number=2				
gene	2239..3552				
	/gene="GVC"				



CDS  
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promoter  
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4548..4583  
/note="multiple cloning site; contains unique restriction  
sites XhoI, SpeI and SmaI"  
4587..5055  
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presented in GenBank Accession Number D21161"  
complement(12801..13133)  
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ORIGIN  
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Best Local Similarity 98.9%; Pred. No. 0;  
Matches 2176; Conservative 0; Mismatches 16; Indels 8; Gaps 3;  
1 AATCCGAAAAGTTTCGACCGGTTTACGTCCTAACTAATATAGGAAAGTGTGCT 60  
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Db 33 AATCCGAAAAGTTTCGACCGGTTTACCGCCCTTAATCAATATATAGGAAAGTGTGCT 92  
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ACCESSION  
VERSION  
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REFERENCE  
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AUTHORS  
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1 (bases 1 to 14230)  
Ouwkerk, P.B., de Kam, R.J., Hoge, J.H. and Meijer, A.H.  
Glucocorticoid-inducible gene expression in rice  
Planta 213 (3), 370-378 (2001)  
11506359  
2 (bases 1 to 14230)  
Ouwkerk, P.B.F.  
Direct Submission  
Submitted (11-AUG-2000) Dept. of Molecular Cell Biology, Institute  
for Molecular Plant Sciences, Wassenaarseweg 64, Leiden 2333 AZ,  
Netherlands  
pINDEX2 is a binary vector designed for glucocorticoid-inducible  
gene expression in plants and is optimized for use in rice; pINDEX2  
is part of a series of four pINDEX vectors (Genbank Accession  
Numbers AF294979-AF294982). pINDEX vectors are based on parts of  
pCAMBIA-1300 encoded by Genbank Accession Number AF234296 and  
pTA7002 (Ioyama, T. and Chua N.-H., 1997, Plant J. 11:605-612).  
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QY      417 TTATAGTTGTGATTCGTTATATTCGACAGTCAATTAAGACATGCTTACTCATCTCAA 476
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ACCESSION	CS055056		
VERSION	CS055056.1	GI:62121528	
KEYWORDS			
SOURCE			
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	Oryza sativa		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.		
REFERENCE	1		
AUTHORS	Broekaert, W., Frankard, V., Hatzfeld, Y. and Mironov, V.		
TITLE	Plants having modified growth characteristics and method for making the same		
JOURNAL	Patent: WO 2005024029-A 15 17-MAR-2005;		
FEATURES	CropDesign N.V. (BE)		
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Best Local Similarity	98.9%;	Pred. No. 0;	
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OY	478	TATTTAGTAAATTAAGACATTTGACTTTATTTATTTATTTATCTTTTTTTCGATTTAGATGC	537
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OY	538	AAGGTACTTAAGCACAACCTTTGTGCTCATGTGCAATGTGTGAGTGCACCTCCTC-ATAA	597
OY	600	CGTTCAACTAGGAGACACATCTCCATATATCACTCGCCTATTTATACATTTAGTATGCAAT	659
OY	558	CGTTCAACTAGGAGACACATCTCTATATATCACTCGCCTATTTATATACATTTAGTATGCAAT	657
OY	660	ATGTGAATTCAGACACTTACCCATCACCAACCAACACTTTTATATATATCTAAAAATACAAA	719
OY	658	ATGTGAATTCAGACACTTACCCATCACCAACCAACACTTTTATATATATCTAAAAATACAAA	717
OY	720	AATATATTTTACAGATATAGCATGAAAGATGAAAGAACTATTTAGTGTCTTTCACATACA	779
OY	718	AATATATTTTACAGATATAGCATGAAAGATGAAAGAACTATTTAGTGTCTTTCACATACA	777
OY	780	AAAAAAGAAAGATTTTGTGTCGTGCGCAGAGCGCAATCTCCCATATTTGGGACAACAGCA	839
OY	778	AAAAAAGAAAGATTTTGTGTCGTGCGCAGAGCGCAATCTCCCATATTTGGGACAACAGCA	837
OY	840	ACAACAGAGTGTGTCGCCACAGAACAAACCAAAAAAGATATCTAACGAGAGACAGC	899
OY	838	ACAACAGAGTGTGTCGCCACAGAACAAACCAAAAAAGATATCTAACGAGAGACAGC	897
OY	900	AAGTCCGACAACCTTTTAAACAGAGGCTTTGGCGCCAGAGAGAGAGAGAGAGGCAAA	959
OY	898	AAGTCCGACAACCTTTTAAACAGAGGCTTTGGCGCCAGAGAGAGAGAGAGAGGCAAA	957
OY	960	GAAGAACCAAGCATCTCTCTCTCCCATCTATTAATTTCTCCCTCTTTTCCCTCTCTAT	1011
OY	958	GAAGAACCAAGCATCTCTCTCTCTCCCATCTATTAATTTCTCCCTCTTTTCCCTCTCTAT	1011
OY	1020	ATAGAGGCAATCCAAAGCCAAAGAGGAGAGACCAAGAGAACGGAACCTAGACAAAGCC	1077
OY	1018	ATAGAGGCAATCCAAAGCCAAAGAGGAGAGACCAAGAGAACGGAACCTAGACAAAGCC	1077

QY 1080 GAGGACCGGCTTTCGATCCATATCTCCGTCGATCTTGGTCGATCTTCCCTC 1139  
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QY 1140 CTCGACCTCTCTCGACAGGSGATGAGCCCTCGATGATCTTGAATTAATGTTGAGG 1199  
DB 1138 CTCGACCTCTCTCGACAGGSGATGAGCCCTCGATGATCTTGGTCGATCTTCCAGG 1197  
QY 1200 TTGTGATGACGGGCGTGTGATGTAAGAAAGGGGATCTGATCTGATGATGATCTGTC 1259  
DB 1198 TTGTGATGACGGGCGTGTGATGTAAGAAAGGGGATCTGATCTGATGATCTGTC 1257  
QY 1260 TTGGATTTGGGATGAGGGGCTTGTGATGTTGATGATGATGATGATGATGATG 1319  
DB 1258 TTGGATTTGGGATGAGGGGCTTGTGATGTTGATGATGATGATGATGATGATG 1317  
QY 1320 TATGCTTTCATCGCTGAGAGCTCTATGAAATGAAATGGTTAAGGTAAGGATCT 1379  
DB 1318 TATGCTTTCATCGCTGAGAGCTCTATGAAATGAAATGGTTAAGGTAAGGATCT 1377  
QY 1380 TCGATTTTGTGATGATCTTGTGATGATGATGATGATGATGATGATGATGATG 1439  
DB 1378 TCGATTTTGTGATGATCTTGTGATGATGATGATGATGATGATGATGATGATG 1436  
QY 1440 TGTATATAAGTACATTTGTGTGCTGATCTGATGATGATGATGATGATGATG 1499  
DB 1437 TGTATATAAGTACATTTGTGTGCTGATCTGATGATGATGATGATGATGATG 1496  
QY 1500 AAGCTATCTTGTGATGATCTTGTGATGATGATGATGATGATGATGATGATG 1559  
DB 1497 AAGCTATCTTGTGATGATCTTGTGATGATGATGATGATGATGATGATGATG 1556  
QY 1560 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1619  
DB 1557 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1616  
QY 1620 GATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1679  
DB 1617 GATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1676  
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QY 1740 TCACCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1799  
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DB 1857 CGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1916  
QY 1920 TGGATTAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1979  
DB 1917 TGGATTAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1975  
QY 1980 AACTGCTCAATTTTGTGATGATGATGATGATGATGATGATGATGATGATG 2039  
DB 1976 AACTGCTCAATTTTGTGATGATGATGATGATGATGATGATGATGATGATG 2035  
QY 2040 CTACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2099  
DB 2036 CTACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2095  
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DB 2096 TGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2155  
QY 2160 TCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2195

DB 2156 TCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2191

RESULT 12  
AR643981  
LOCUS AR643981 898 bp DNA linear PAT 20-APR-2005  
DEFINITION Sequence 50 from patent US 6867293.  
ACCESSION AR643981  
VERSION AR643981.1 GI:62782641  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 898)  
AUTHORS Andrews,C.J., Bachoo,S., Hawkes,T.R., Pickerill,A.P. and Warner,S.A.J.  
TITLE polynucleotide constructs having at least one transcriptional enhancer and encoding a modified rice BRSPS enzyme  
JOURNAL Patent: US 6867293-A 50 15-MAR-2005;  
Syngenta limited; Gulliford;  
WOX;  
FEATURES  
source location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 39.5%; Score 867.2; DB 6; Length 898;  
Best Local Similarity 99.2%; Pred. No. 3,9e-147;  
Matches 893; Conservative 0; Mismatches 3; Indels 4; Gaps 2;

QY 1 AATCGGAAAGTTTGTGACCGCTTTCAGCTCTAATCAATATAGGAAAGTGTGCT 60  
DB 2 AATCGGAAAGTTTGTGACCGCTTTCAGCTCTAATCAATATAGGAAAGTGTGCT 61  
QY 61 AATATATAAGTACCTTATATATATGAGCGCTGATTAATGAACTATGAAAGAACT 120  
DB 62 AATATATAAGTACCTTATATATATGAGCGCTGATTAATGAACTATGAAAGAACT 121  
QY 121 CATCACTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 180  
DB 122 CATCACTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 181  
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QY 301 AAAAAATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 360  
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QY 361 AGAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
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QY 421 AGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
DB 419 AGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 478  
QY 481 TATTTAGTATTAAGACATGATGATGATGATGATGATGATGATGATGATGATG 540  
DB 479 TATTTAGTATTAAGACATGATGATGATGATGATGATGATGATGATGATGATG 538  
QY 541 AAGGTAAGTACGACACACTTGTGCTCATGATGATGATGATGATGATGATGATG 599  
DB 539 AAGGTAAGTACGACACACTTGTGCTCATGATGATGATGATGATGATGATGATG 598  
QY 600 CGTTCACTAGGACACATCTTCATATCACTGCTATTTAATATCAATTAAGTACAT 659

|||||  
Db CCTCAACTAGGACACATCTCTAATATCACTCGCTATTATATCATTTAGTAGCAAT 658  
Qy 660 ATCTGAATTCAGACCTTCACATACACGACCACTTTAATATATCAATATCAAAA 719  
Db 659 ATCTGAATTCAGACCTTCACATACACGACCACTTTAATATATCAATATCAAAA 718  
Qy 720 AATAATTTTACAGATAGCATGATAAGTATGAAACGAACTATTAGTTTTTCAATACA 779  
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Db 779 AAAAAAAAAAAGATTTTCTGCTGCGCGGCGCAATCTCCATATTGGGACACAGGCA 838  
Qy 840 ACAACAGAGTGCTGCCACAGAACCAACCAAAAAAGATGATCTACGAGGACAGC 899  
Db 839 ACAACAGAGTGCTGCCACAGAACCAACCAAAAAAGATGATCTACGAGGACAGC 898

## RESULT 13

AX044095 898 bp DNA linear PAT 24-NOV-2000  
LOCUS Sequence 50 from Patent WO0066748.  
DEFINITION AX044095  
ACCESSION AX044095  
VERSION AX044095.1 GI:11342973  
KEYWORDS

## SOURCE

Oryza sp.  
Oryza sp.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

1 Hawkes, T.R., Warner, S.A., Andrews, C.J., Bachoo, S. and  
Pickett, J.L.A.P.  
Herbicide resistant plants  
Patent: WO 0066748-A 50 09-NOV-2000;  
ZENECA LIMITED (GB)

## FEATURES

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/mol\_type="unassigned DNA"  
/db\_xref="taxon:52841"

## ORIGIN

Query Match 39.5%; Score 867.2; DB 6; Length 898;  
Best Local Similarity 99.2%; Pred. No. 3.9e-147;  
Matches 893; Conservative 0; Mismatches 3; Indels 4; Gaps 2;

Qy 1 AATCGGAAAAGTTTCTGACCGTTTTCAGCTCTAATCAATATAGGAACTGTGCT 60  
Db 2 AATCGGAAAAGTTTCTGACCGTTTTCAGCTCTAATCAATATAGGAACTGTGCT 61  
Qy 61 AATATATAAATGAGACCTTATATATGTAGCGCTGATTAAGTAATGAAAACT 120  
Db 62 AATATATAAATGAGACCTTATATATGTAGCGCTGATTAAGTAATGAAAACT 121  
Qy 121 CATCAACCTACTTATAGTGGCAATCGGCTAAATAAAAGATCGTACATAGTTTCT 180  
Db 122 CATCAACCTACTTATAGTGGCAATCGGCTAAATAAAAGATCGTACATAGTTTCT 181  
Qy 181 TTTCTTAGTAAATTAAGTGGGAAAATGAATCATTTTCTTGAATATACGTTCAATC 240  
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Qy 301 AAAAAATCTTTCTAGTGAATCAATGAGTAAAGAGATTTTTTTTAAAAAAAAT 360  
Db 302 AAAAAATCTTTCTAGTGAATCAATGAGTAAAGAGATTTTTTTTAAAAAAAAT 358

Qy 361 AGAATGAAGATATTCTGACGATATCGGCAAGATTTAAACATATATATATATTTAT 420  
Db 359 AGAATGAAGATATTCTGACGATATCGGCAAGATTTAAACATATATATATATTTAT 418  
Qy 421 AGTTGATGATTCGTTATATGACAGTATTAAGGACATGCTTACTCATCTCAATTT 480  
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Qy 481 TATTAGTAAATTAAGACAAATGACTTATTTTATATTTATATTTTCTTTTGCATTAAGATGC 540  
Db 479 TATTAGTAAATTAAGACAAATGACTTATTTTATATATATATTTTCTTTTGCATTAAGATGC 538  
Qy 541 AAGGACTTATGACACACCTTTGCTCATGTGCAATGTGTAGAGACACTCTC-ATAACA 599  
Db 539 AAGGACTTATGACACACCTTTGCTCATGTGCAATGTGTAGAGACACTCTC-ATAACA 598  
Qy 600 CGTTCAACTAGGACACATCTCCAAATATACATCGCTATTATATACATTTAGTAGCAAT 659  
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Qy 660 ATCTGAATTCAGACCTTCACATACACGACCACTTTAATATATCTAAATACAAAA 719  
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Qy 840 ACAACAGAGTGCTGCCACAGAACCAACCAAAAAAGATGATCTACGAGGACAGC 899  
Db 839 ACAACAGAGTGCTGCCACAGAACCAACCAAAAAAGATGATCTACGAGGACAGC 898

## RESULT 14

AX044183 898 bp DNA linear PAT 24-NOV-2000  
LOCUS Sequence 35 from Patent WO0066746.  
DEFINITION AX044183  
ACCESSION AX044183  
VERSION AX044183.1 GI:11343061  
KEYWORDS

## SOURCE

Oryza sp.  
Oryza sp.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

1 Hawkes, T.R., Warner, S.A., Andrews, C.J., Bachoo, S. and  
Pickett, J.L.A.P.  
Herbicide resistant plants  
Patent: WO 0066746-A 35 09-NOV-2000;  
ZENECA LIMITED (GB)

## FEATURES

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/organism="Oryza sp."  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:52841"

## ORIGIN

Query Match 39.5%; Score 867.2; DB 6; Length 898;  
Best Local Similarity 99.2%; Pred. No. 3.9e-147;  
Matches 893; Conservative 0; Mismatches 3; Indels 4; Gaps 2;

Qy 1 AATCGGAAAAGTTTCTGACCGTTTTCAGCTCTAATCAATATAGGAACTGTGCT 60  
Db 2 AATCGGAAAAGTTTCTGACCGTTTTCAGCTCTAATCAATATAGGAACTGTGCT 61  
Qy 61 AATATATAAATGAGACCTTATATATGTAGCGCTGATTAAGTAATGAAAACT 120  
Db 62 AATATATAAATGAGACCTTATATATGTAGCGCTGATTAAGTAATGAAAACT 121





Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K.,  
Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M.,  
Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,  
Takeku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,  
Yasunishi,A. and Hayashizaki,Y.

# FEATURES

Source  
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/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nipponbare"  
/db\_xref="taxon:39947"  
/clone="U013170105"

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Query Match 5.7%; Score 124.2; DB 15; Length 752;  
Best Local Similarity 97.2%; Pred. No. 2.2e-12;  
Matches 137; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
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Db 5 GGAGGCATCCAAAGCCAAAGAGGAGAGACCAAGACCGGACTAGCAGAGCCGAG 64  
Oy 1083 GGACGGCCTTCTTCGATCCATATCTTCGGGTGAGTTCTTGATCGATCTTCCCTCCTC 1142  
|||  
Db 65 GGACGGCC-TCTCGATCCATATCTTCGGGTGAGTTCTTGATCGATCTTCCCTCCTC 123  
Oy 1143 CACCTCTCTCTCAGAGGTAT 1163  
|||  
Db 124 CACCTCTCTCTCAGAGTTCT 144

Search completed: April 21, 2006, 15:46:39  
Job time : 10747 secs



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 21, 2006, 08:53:40 ; Search time 1226 Seconds  
(Without alignments)  
11932.300 Million cell updates/sec

Title: US-10-541-315-1

Perfect score: 2195  
Sequence: 1 aatcgcgaagaattcttcacac.....cacttcaccagcaaatc 2195

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 333346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_21.\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2195	100.0	2195	13	ADRO1013 Regulator
2	2139.2	97.5	3032	13	ADT92083
3	2133.4	97.2	9361	3	ADAO1285
4	2133.4	97.2	10629	3	AAAD01286
5	2115.2	96.4	2191	14	ADY69039
6	867.2	39.5	898	3	AAC88400
7	867.2	39.5	898	3	AAC87195
8	126.8	5.8	719	10	ADK5377
9	126.8	5.8	724	10	ADDI6740
10	126.8	5.8	725	10	ADK59227
11	126.8	5.8	782	10	ADDI7562
12	126.8	5.8	808	12	ADU39051
13	84.6	3.9	2000	11	ACU36783
14	61.2	2.8	2000	11	ACU38652
15	55.6	2.5	101954	13	ABD33574
16	55.4	2.5	8056	8	ABZ10246
17	55.2	2.5	612	14	ACI64894
18	55.2	2.5	5379	6	ABL3676
19	55.2	2.5	5379	6	ABL34576

20	55.2	2.5	5379	6	ABL70369	Ab170369 Chemical1
21	55.2	2.5	5379	7	AD899837	Ad899837 Bisulphic
22	55	2.5	69081	11	ACN44642	ACN44642 Human gen
23	54.8	2.5	2482	14	AD271091	Ad271091 Human chr
24	54.4	2.5	16766	6	ABK34156	Ab134156 Human imm
25	53.8	2.5	9760	6	ABK31242	Abk31242 Signal tr
26	53.8	2.5	9760	6	ABK70197	Ab170197 Chemical1
27	53.8	2.5	9760	6	AA661155	AA661155 Human gen
28	53.6	2.5	47108	6	ABK31511	Abk31511 Signal tr
29	53.6	2.4	700	4	AAH93026	AAH93026 Human inf
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31	53.2	2.4	2000	11	ACI37108	ACI37108 Rice stre
32	53.2	2.4	2501	14	ADY98099	AdY98099 Bisulfite
33	52.6	2.4	8076	6	ABK39955	AbK39955 Human che
34	52.6	2.4	8136	6	ABK39957	AbK39957 Human che
35	52.6	2.4	8136	6	ABK32555	Ab132555 Human imm
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39	51.6	2.4	2131	14	AD271009	Ad271009 Human chr
40	51.6	2.4	8056	8	AB210100	Ab210100 Haematopo
41	51.6	2.4	147300	12	ADP45593	AdP45593 Human rho
42	51.6	2.4	147700	14	ADX98570	AdX98570 Human gua
43	51.4	2.3	5979	4	AA645313	AA645313 Chemical1
44	51.4	2.3	5979	6	ABK28152	AbK28152 DNA trans
45	51.4	2.3	7341	6	ABQ67109	AbQ67109 Human ang

## ALIGNMENTS

RESULT 1	ADRO1013	ADRO1013 standard; DNA; 2195 BP.
ID	ADRO1013	
AC	ADRO1013	
XX		
DT	21-OCT-2004 (first entry)	
XX		
DE	Regulatory DNA sequence of the rice GOS2 gene SeqID 1.	
KW	regulatory; plant; rice; GOS2; non-monocotyledonous; transgenic; ds.	
OS	Oryza sativa.	
XX		
PN	WO2004065596-A2.	
XX		
PD	05-AUG-2004.	
XX		
PF	21-JAN-2004; 2004WO-EP000645.	
XX		
PR	21-JAN-2003; 2003BP-00075207.	
XX		
PA	(CROP-) CROPPESIGN NV.	
PI	Hatzfeld Y, Inze D;	
XX		
DR	WPI; 2004-562175/54.	
XX		
PT	Use of a regulatory nucleic acid sequence for driving expression of an associated nucleic acid sequence in a non-monocotyledonous plant or plant cell.	
XX		
PS	Claim 1; SEQ ID NO 1; 25pp; English.	
XX		
CC	This invention relates to a novel isolated regulatory nucleic acid sequence that is useful in the field of plant molecular biology.	
CC	Specifically, it refers to a regulatory gene of the rice GOS2 gene that can drive expression of an associated nucleic acid sequence in a non-monocotyledonous plant or plant cell.	
CC	The present invention describes introducing a regulatory sequence that results in constitutive expression (with levels similar to that of CamV 35S) of an isolated or endogenous nucleic acid sequence in a transgenic non-monocotyledonous plant. In	

CC particular, a plant cell derived from either a fodder or forage legume,  
CC ornamental plant, food crop, tree or shrub, preferably from cotton,  
CC potato, tomato, cabbage, sugar beet, soybean, sunflower, or peas. This  
CC polynucleotide sequence is the regulatory sequence of the rice GOS2 gene  
CC of the invention.

XX  
SQ Sequence 2195 BP; 639 A; 426 C; 403 G; 727 T; 0 U; 0 Other;

Query Match 100.0%; Score 2195; DB 13; Length 2195;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AAATATAAAATGAGACCTTATATATGTACCGCTGATTAAGAACTATATAGAAAACCT 120
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DB 121 CATCCACTACTTATAGTGGCAATCGGGCTAAATPAAAAGAGCGCTACACTAGTTTGGT 180
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DB 301 AAAAAATCTTTTACGTGAACTCAATGGGTAAAGAGAGATATTTTTTTTTAAAAAAAT 360
QY 361 AGAATGAAAGATATCTGAAAGTATCGGCAAGATTTTAAACATATATATATATATTTAT 420
DB 361 AGAATGAAAGATATCTGAAAGTATCGGCAAGATTTTAAACATATATATATATATTTAT 420
QY 421 AGTTTGTGATTCGTATATATCGCAAGTCAATTAAGAGCATGTCTTACCTCATATTTT 480
DB 421 AGTTTGTGATTCGTATATATCGCAAGTCAATTAAGAGCATGTCTTACCTCATATTTT 480
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DB 481 TATTTAGTAATTAAGACAATGACTTATTTTATATATATATCTTTTTCGATTAGATGC 540
QY 541 AAGGTAATTAAGACAATGACTTGTGCTCATGTGCAATGTGTAGTGACCTCTCATATAC 600
DB 541 AAGGTAATTAAGACAATGACTTGTGCTCATGTGCAATGTGTAGTGACCTCTCATATAC 600
QY 601 GTTCAACTAGCGACACATCTCCAAATATCACTGGCCCTATTAATACCTTAAAGTAA 660
DB 601 GTTCAACTAGCGACACATCTCCAAATATCACTGGCCCTATTAATACCTTAAAGTAA 660
QY 661 TCTGAATTAAGACACTTCAATCAACAGACCACTTTTATATATATCTAAATACAAA 720
DB 661 TCTGAATTAAGACACTTCAATCAACAGACCACTTTTATATATATCTAAATACAAA 720
QY 721 ATATATTTTACAGATATAGCATGAAGATGAAGCAAGATATTAAGTATTTTCAATACA 780
DB 721 ATATATTTTACAGATATAGCATGAAGATGAAGCAAGATATTAAGTATTTTCAATACA 780
QY 781 AAAAAAAGAAATTTTGTGTCGTGCGGAGGCCAATCTCCCATATTTGGGACACAGGCA 840
DB 781 AAAAAAAGAAATTTTGTGTCGTGCGGAGGCCAATCTCCCATATTTGGGACACAGGCA 840
QY 841 CAACAGAGTGGCTGCCACAGAACCAACCAAAAAAGATGATCTTAACGAGAGACAGCA 900
DB 841 CAACAGAGTGGCTGCCACAGAACCAACCAAAAAAGATGATCTTAACGAGAGACAGCA 900
QY 901 ACTCGCAACAACTTTTAAACAGCAGGCTTTTGGCCAGAGAGAGAGAGAGGCAAG 960
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DB 901 ACTCGCAACAACTTTTAAACAGCAGGCTTTTGGCCAGAGAGAGAGAGAGGCAAG 960
QY 961 AAAACCAAGCATCTCTCTCTCCATCTATAAATCTCTCCCTTTTCCCTCTCTATA 1020
DB 961 AAAACCAAGCATCTCTCTCTCCATCTATAAATCTCTCCCTTTTCCCTCTCTATA 1020
QY 1021 TAGAGGCAATCCAGACCAAGAAAGAGAGACCAAGAGACACGGACTATAGAGAGCCG 1080
DB 1021 TAGAGGCAATCCAGACCAAGAAAGAGAGACCAAGAGACACGGACTATAGAGAGCCG 1080
QY 1081 AGCGACCGCTTCTTCCATCCATATCTTCCGTCAGTTCTTGGTCGATCTCTCCCTCC 1140
DB 1081 AGCGACCGCTTCTTCCATCCATATCTTCCGTCAGTTCTTGGTCGATCTCTCCCTCC 1140
QY 1141 TCCACTCTCTCTCACAGAGGTAATGACCCTTCGAGTTGCTTGAATTAATTTCTAGAT 1200
DB 1141 TCCACTCTCTCTCACAGAGGTAATGACCCTTCGAGTTGCTTGAATTAATTTCTAGAT 1200
QY 1201 TGTGTAGTACGGGCGTTGATGTTAGAAAAGGGATCTGTATCTGTATGATTTCTGTCT 1260
DB 1201 TGTGTAGTACGGGCGTTGATGTTAGAAAAGGGATCTGTATCTGTATGATTTCTGTCT 1260
QY 1261 TGGATTTGGAGTATAGGGGCTTCTGTATGTGATGTATCGGTTCCGTTGATTAGTAT 1320
DB 1261 TGGATTTGGAGTATAGGGGCTTCTGTATGTGATGTATCGGTTCCGTTGATTAGTAT 1320
QY 1321 ATGTTTTCAATCGCTGAGAGCTCTATGGAATGAAGATGTTAAGGTTACGAAATCTT 1380
DB 1321 ATGTTTTCAATCGCTGAGAGCTCTATGGAATGAAGATGTTAAGGTTACGAAATCTT 1380
QY 1381 GCGATTTTGTGAGTACCTTTTGTGTTAGTAAATCAGAGACCGGTATTTTGTGTGT 1440
DB 1381 GCGATTTTGTGAGTACCTTTTGTGTTAGTAAATCAGAGACCGGTATTTTGTGTGT 1440
QY 1441 GTAATTAAGTATCATTTTGTGTCTCGATTTCTGTATGTATGCTTCTCATTTGAGCA 1500
DB 1441 GTAATTAAGTATCATTTTGTGTCTCGATTTCTGTATGTATGCTTCTCATTTGAGCA 1500
QY 1501 AGCTATCTTGTGTTATTTCCCTATGAAACAAAATATCCAACTTTGAAAGACGCTCCGT 1560
DB 1501 AGCTATCTTGTGTTATTTCCCTATGAAACAAAATATCCAACTTTGAAAGACGCTCCGT 1560
QY 1561 TGATGAGATGTAATGATTTCTTAAGCTGTGCCAAATTTTCCGAGCTGCTGTATAG 1620
DB 1561 TGATGAGATGTAATGATTTCTTAAGCTGTGCCAAATTTTCCGAGCTGCTGTATAG 1620
QY 1621 ATACGTAAGTCCCATCAAGAAATTCATGAAGACGTTATATCTCTCAGAGAACAGGGAT 1680
DB 1621 ATACGTAAGTCCCATCAAGAAATTCATGAAGACGTTATATCTCTCAGAGAACAGGGAT 1680
QY 1681 TCCCTGTTCTCCGATTTGCTTATAGTCCAGAAATTTTTCCTCCAAATATCTTAAAAAGT 1740
DB 1681 TCCCTGTTCTCCGATTTGCTTATAGTCCAGAAATTTTTCCTCCAAATATCTTAAAAAGT 1740
QY 1741 CACTTTCGATTCAGTTCAATGAATGATGCTACAAATTAATGCTTTATAGCGTTATCC 1800
DB 1741 CACTTTCGATTCAGTTCAATGAATGATGCTACAAATTAATGCTTTATAGCGTTATCC 1800
QY 1801 TAGCTGTAGTCAAGTTATAGGTAATACCCCTATATGTTTATAGTACAGAGAAACCTATCC 1860
DB 1801 TAGCTGTAGTCAAGTTATAGGTAATACCCCTATATGTTTATAGTACAGAGAAACCTATCC 1860
QY 1861 GATTTCTGATCTCCATTTTATATATATATATATATATATATATATATATATATATAT 1920
DB 1861 GATTTCTGATCTCCATTTTATATATATATATATATATATATATATATATATATATAT 1920
QY 1921 GATTAATTTTATATATATATATATATATATATATATATATATATATATATATATAT 1980
DB 1921 GATTAATTTTATATATATATATATATATATATATATATATATATATATATATATAT 1980
QY 1981 ACTGTCCTCAATTTTGTGTTTCAATTCATGATATATATATATATATATATATATATAT 2040
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DB 1981 ACTGTCCTCAATTTTGGTTTCAAAATTCACATGATATCTATGATTAATCTCTTGTATC 2040  
QY 2041 TACCTGTAGAAAGTTCTTTGGTTATTCCTTGATCTTGATTCAGAAAGAAATTTAT 2100  
DB 2041 TACCTGTAGAAAGTTCTTTGGTTATTCCTTGATCTTGATTCAGAAAGAAATTTAT 2100  
QY 2101 GAAGCTGTAAATCGGAGTAAGTATTAAGTCTGTCTTAAATTCATTTCTTTGTGCAATT 2160  
DB 2101 GAAGCTGTAAATCGGAGTAAGTATTAAGTCTGTCTTAAATTCATTTCTTTGTGCAATT 2160  
QY 2161 CTGCTGTATGCTTGGCCATCTTTCACCGCAAGATTC 2195  
DB 2161 CTGCTGTATGCTTGGCCATCTTTCACCGCAAGATTC 2195  
RESULT 2  
ID ADT92083 standard; DNA; 3032 BP.  
XX  
AC ADT92083;  
XX  
DT 13-JAN-2005 (first entry)  
XX  
DB PRO0129-CD51585 expression cassette for MT2a.  
XX  
KM MT2a; plant growth; plant development; transgenic; genetic modification;  
XX metallochionein; metal accumulation; abiotic stress; growth regulator;  
KM gene; ss.  
XX  
OS Synthetic.  
XX  
PN WO2004090142-A2.  
XX  
PD 21-OCT-2004.  
XX  
PP 14-APR-2004; 2004WO-EP050519.  
XX  
PR 14-APR-2003; 2003EP-00076086.  
XX  
PA (CROP-) CROPBDSIGN NV.  
XX  
PI Sanz Molinero AI;  
XX  
DR WPI; 2004-748770/73.  
XX  
PT Modifying plant growth and development for altering growth  
PT characteristics in plants, comprises introducing a genetic modification  
PT in the plant and selecting modulated expression of a nucleic acid  
PT encoding a metallochionein protein.  
XX  
PS Claim 13; SEQ ID NO 7; 49pp; English.  
XX  
XX The invention relates to modifying plant growth and development and  
CC involves introducing a genetic modification in the plant and selecting  
CC for modulated expression in the plant of a nucleic acid encoding a  
CC metallochionein protein, provided that the modified growth and  
CC development is not increased metal accumulation or increased tolerance or  
CC resistance to abiotic stress. In modifying plant growth and development,  
CC the modified plant growth and development is increased yield, preferably  
CC an increase of biomass and/or seed yield, when compared to corresponding  
CC wild type plants. Genetic modification comprises introducing an isolated  
CC nucleic acid encoding a metallochionein protein into a plant. The nucleic  
CC acid encoding a metallochionein protein encodes a type 2 metallochionein  
CC and is derived from a plant, preferably a dicotyledonous plant, more  
CC preferably from the family Brassicaceae, e.g. Arabidopsis thaliana. The  
CC expression of the nucleic acid encoding a metallochionein is driven by a  
CC constitutive promoter, preferably the rice GOS2 promoter. The  
CC metallochionein protein and its homologues, derivatives, and active  
CC fragments, and the encoding polynucleotides are useful for modifying the  
CC growth characteristics of plants, provided that the modified growth and  
CC development is not increased metal accumulation or increased tolerance or  
CC resistance to abiotic stress. They are also useful as a growth regulator.  
CC The method is useful for modifying plant growth and development. It is

CC also useful for producing plants with altered growth characteristics,  
CC e.g. increased yield, increased biomass, increased total above ground  
CC area, increased plant height, increased number of tillers, increased  
CC number of primary panicles, increased total number of seeds, or increased  
CC harvest index. The present sequence represents the nucleotide sequence of  
CC an FRO0129-CD51585 -zein and IBCS deltaC4 double terminator expression  
CC cassette for the expression of A. thaliana AtMT2a gene.  
XX  
SQ Sequence 3032 BP; 917 A; 595 C; 581 G; 939 T; 0 U; 0 Other;  
Query Match 97.5%; Score 2139.2; DB 13; Length 3032;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 2174; Conservative 0; Mismatches 18; Indels 4; Gaps 2;  
QY 1 AATCGAAAGTTTCTGACCGTTTCACTGCTTAATCAATATAGGAAACGTGTCT 60  
DB 1 AATCGAAAGTTTCTGACCGTTTCACTGCTTAATCAATATAGGAAACGTGTCT 60  
QY 61 AAATATAAATGAGACCTTAATATATGATGCGCTGATTAATAGAACTATGTAAGAAACT 120  
DB 61 AAATATAAATGAGACCTTAATATATGATGCGCTGATTAATAGAACTATGTAAGAAACT 120  
QY 121 CATCCACTACTTATGATGCGCAATCGGCTAAATTAAGAGTGGCTACCTAGTTTGT 180  
DB 121 CATCCACTACTTATGATGCGCAATCGGCTAAATTAAGAGTGGCTACCTAGTTTGT 180  
QY 181 TTTCTGTATTAATTAAGTGGGAAATGAATCATATATGCTTGAATATAGCTTACATC 240  
DB 181 TTTCTGTATTAATTAAGTGGGAAATGAATCATATATGCTTGAATATAGCTTACATC 240  
QY 241 TCTGTATGAATTAATTAATTAATGAGTATGATGATCAATCACTCTTCTTGAATA 300  
DB 241 TCTGTATGAATTAATTAATTAATGAGTATGATGATCAATCACTCTTCTTGAATA 300  
QY 301 AAAAAATCTTTCTAGCTGAATCAATGGTAAAGAGATATTTTAAAAAAT 360  
DB 301 AAAAAATCTTTCTAGCTGAATCAATGGTAAAGAGATATTTTAAAAAAT 360  
QY 361 AAAAAATCTTTCTAGCTGAATCAATGGTAAAGAGATATTTTAAAAAAT 360  
DB 361 AAAAAATCTTTCTAGCTGAATCAATGGTAAAGAGATATTTTAAAAAAT 360  
QY 421 AGTTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480  
DB 421 AGTTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480  
QY 481 TATTTAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540  
DB 481 TATTTAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540  
QY 541 AAGGACTTACGACACACTTGTGCTGATGATGATGATGATGATGATGATGATGATGAT 599  
DB 541 AAGGACTTACGACACACTTGTGCTGATGATGATGATGATGATGATGATGATGATGAT 599  
QY 600 CGTTCACTAGGACACATCTTCATATCACTGCTTATTAATCAATTAAGTATGAT 659  
DB 600 CGTTCACTAGGACACATCTTCATATCACTGCTTATTAATCAATTAAGTATGAT 659  
QY 658 ATCTGAATTCAGACCTTCACTGATCAACGACCACTTTTAAATATCTAAATCAAAA 717  
DB 658 ATCTGAATTCAGACCTTCACTGATCAACGACCACTTTTAAATATCTAAATCAAAA 717  
QY 720 AATATTTTACAGATAGATGAAGAAAGTATGAAGAAAGTATGAAGTATGAAGTATGAAG 779  
DB 720 AATATTTTACAGATAGATGAAGAAAGTATGAAGAAAGTATGAAGTATGAAGTATGAAG 779  
QY 778 AAAAAAAGAAATTTTCTGCTGCGGACGACCAATCTCCATATTTGGGACACAGGCA 839  
DB 778 AAAAAAAGAAATTTTCTGCTGCGGACGACCAATCTCCATATTTGGGACACAGGCA 839  
QY 840 ACAACAGATGCTGCTCCACAGAACACCCCAAAAAACGATGATTAACGAGAGACAGC 899  
DB 840 ACAACAGATGCTGCTCCACAGAACACCCCAAAAAACGATGATTAACGAGAGACAGC 899  
QY 897 AAAAAAAGAAATTTTCTGCTGCGGACGACCAATCTCCATATTTGGGACACAGGCA 957  
DB 897 AAAAAAAGAAATTTTCTGCTGCGGACGACCAATCTCCATATTTGGGACACAGGCA 957

QY	900	AAGTCGCGAACAACCTTTTAA	CAGGAGGCTTTGGGGCCAGGAGGAGGAGGCGCAA	959
Db	898	AAGTCGCGAACAACCTTTTAA	CAGGAGGCTTTGGGGCCAGGAGGAGGAGGAGGCGCAA	957
QY	960	GAAGAACCAAGATCCTCCTCCT	CCCATCTAAATTCCTCCGCCCTTTTCCCTCTCAT	1019
Db	958	GAAGAACCAAGATCCTCCTCCT	CCCATCTAAATTCCTCCGCCCTTTTCCCTCTCAT	1017
QY	1020	ATAGGAGGCATCCAAAGC	CAAGAGGAGGAGACACCAAGGACAGCGCATAGCAAGACC	1079
Db	1018	ATAGGAGGCATCCAAAGC	CAAGAGGAGGAGACACCAAGGACAGCGCATAGCAAGACC	1077
QY	1080	GAGGAGCCGCTTCTTGAT	CTCATATCTTCGGGTGAGTTCTTGGTGGATCTCTTCCCTC	1139
Db	1078	GAGGAGCCGCTTCTTGAT	CTCATATCTTCGGGTGAGTTCTTGGTGGATCTCTTCCCTC	1137
QY	1140	CTCCACCTCTCTCA	CAGGGATGTCCTTCGGTTGTTTGAATTTATGTTCTTAGG	1199
Db	1138	CTCCACCTCTCTCTCA	CAGGGATGTCCTTCGGTTGTTTGAATTTATGTTCTTAGG	1197
QY	1200	TTTGTTGATACGGGCGCT	GATTGTTAGAAAGGGATCTGTATCTGTATGATTTCTCTGTC	1259
Db	1198	TTTGTTGATACGGGCGCT	GATTGTTAGAAAGGGATCTGTATCTGTATGATTTCTCTGTC	1257
QY	1260	TTGATTTGGGATAGAGGG	TTCTTGATGTCATGTAATGAGTTCCGTTTGAATTAGTAG	1319
Db	1258	TTGATTTGGGATAGAGGG	TTCTTGATGTCATGTAATGAGTTCCGTTTGAATTAGTAG	1317
QY	1320	TATGTTTTCATGCTGCT	GAGAGCTCTATGAAATGAAATGTTTAGGGTACGGAATCT	1379
Db	1318	TATGTTTTCATGCTGCT	GAGAGCTCTATGAAATGAAATGTTTAGGGTACGGAATCT	1377
QY	1380	TGGCATTTTGAGAGACCT	TTTGTGTTGAGTAAATCAGACACCGGATTTTGCTTGG	1439
Db	1378	TGGCATTTTGAGAGACCT	TTTGTGTTGAGTAAATCAGACACCGGATTTTGCTTGG	1437
QY	1440	TGTAATAAAGATCACTT	GTGTGGCTCCGATCTCTGAGTAGATGCTTCTCGATTTGACG	1499
Db	1438	TGTAATAAAGATCACTT	GTGTGGCTCCGATCTCTGAGTAGATGCTTCTCGATTTGACG	1497
QY	1500	AAGCTATCTTTGTTTAT	TTCCTTATGAAACAAATAATCCACTTTGAGACGCTCCCG	1559
Db	1498	AAGCTATCTTTGTTTAT	TTCCTTATGAAACAAATAATCCACTTTGAGACGCTCCCG	1557
QY	1560	TTGATGAGATGGAATGA	TTGATTTCTTAGCCCTGTCCAAATTTTGGCAGCTGGCTGTGTTA	1619
Db	1558	TTGATGAGATGGAATGA	TTGATTTCTTAGCCCTGTCCAAATTTTGGCAGCTGGCTGTGTTA	1617
QY	1620	GATACAGATGCCCATC	ACAGAAATTCATGAAACAGTTATATCTTCAGGACAGGGGA	1679
Db	1618	GATACAGATGCCCATC	ACAGAAATTCATGAAACAGTTATATCTTCAGGACAGGGGA	1677
QY	1680	TTCCCTGTTCTCCGAT	TTCCTTAGTCCCAAGAAATTTTTTTTCCCAATATCTTAAAG	1739
Db	1678	TTCCCTGTTCTCCGAT	TTCCTTAGTCCCAAGAAATTTTTTTTCCCAATATCTTAAAG	1737
QY	1740	TCACTTTCTGATGATCA	GTTCANATGTAATGTAATATGCTTTATAGGCTATC	1799
Db	1738	TCACTTTCTGATGATCA	GTTCANATGTAATGTAATATGCTTTATAGGCTATC	1797
QY	1800	CTAGCTGATGATCA	GTTCATATAGGATATACCCCTATAGTTTATGTCAGAGAAAGACTTATC	1859
Db	1798	CTAGCTGATGATCA	GTTCATATAGGATATACCCCTATAGTTTATGTCAGAGAAAGACTTATC	1857
QY	1860	CGATTTCTGATCTCCAT	TTTATTAATTAATGAAATGAACTGTAGCATTAAGCATTTTCAT	1919
Db	1858	CGATTTCTGATCTCCAT	TTTATTAATTAATGAAATGAACTGTAGCATTAAGCATTTTCAT	1917
QY	1920	TGGAATATTTTTTTTAT	TATAGCTTCAACCCCTTCATATTTGAGCTGAAATCTGGGATG	1979
Db	1918	TGGAATATTTTTTTTAT	TATAGCTTCAACCCCTTCATATTTGAGCTGAAATCTGGGATG	1977

Qy	1980	AACGTCCTCAATTTTGGTTTCAAAATTCACATTCATTATCTATGATATCTCTTGAT	2033
Dy	1978	AACGTCTCAATTTTGGTTTCAAAATTCACATTCATTATCTATGATATCTCTTGAT	2031
Oy	2040	CTACCTGTAGAAAGTTTCTTTTGGTTATCTTGAATCGTCTGATTTACGAAAGAAATTTA	2099
Dy	2038	CTACCTGTAGAAAGTTTCTTTTGGTTATCTTGAATCGTCTGATTTACGAAAGAAATTTA	2097
Oy	2100	TGAAGCTGTATCGGGATAGTTATATACGCTGTCTTATGATTCATTTCTTTGGCAGT	2159
Dy	2098	TGAAGCTGTATCGGGATAGTTATATACGCTGTCTTATGATTCATTTCTTTGGCAGT	2157
Oy	2160	TCTTGGTGTAGCTTGGCACTTTCACGCAAGAAAGTTTC	2195
Dy	2158	TCTTGGTGTAGCTTGGCACTTTCACGCAAGAAAGTTTC	2193
Db			
RESULT 3			
ID	AAD01285/c		
XX	AAD01285 standard; DNA; 9361 BP.		
XX	AAD01285;		
XX	12-OCT-2000 (first entry)		
XX			
XX	Rice transformation vector; pGOS2-hpt.		
XX	Matrix Attachment Region; MAR; rice transformation vector; pGOS2-hpt;		
XX	scaffold attachment region; gene expression; transgenic organism; ds.		
XX	Synthetic.		
XX	WO200032800-A1.		
XX	08-JUN-2000.		
XX	30-NOV-1999; 99WO-US028123.		
XX	01-DEC-1998; 98US-0110437P.		
XX	(DOMC ) DOM AGROSCIENCES LLC.		
XX	Van Der Geest AHM, Ainley WM, Cowen NM, Welter ME, Woosley AT;		
XX	WPI; 2000-412345/35.		
XX			
XX	An isolated DNA molecule for use as a matrix attachment region to		
XX	increase expression of genes introduced in transformed plants comprises a		
XX	298 base pair sequence described in the specification.		
XX			
XX	Example 3; Page 48-51; 73pp; English.		
XX			
XX	The patent discloses a DNA molecule, useful as matrix attachment region		
XX	(MAR) or scaffold attachment region, to increase the expression of genes		
XX	introduced in transformed plants. MARS are located in non-transcribed		
XX	regions of genes and form the physical boundaries of individual DNA		
XX	loops. They are rich in adenosine and thymine bases and contain certain		
XX	conserved sequence elements and structural features. They are about 300-		
XX	2000 bp in length. Increased levels of expression of DNA introduced into		
XX	plants can be achieved by use of MAR. They can also reduce the position		
XX	effect in transgenic organisms. The present DNA sequence is the rice		
XX	transformation vector pGOS2-hpt, that contains a hygromycin selectable		
XX	marker driven by the 35S promoter and a GOS2/GUS/nos cassette (GOS2		
XX	transcription initiation region/GUS structural gene/nos 3' untranslated		
XX	region). The GOS2 transcription initiation region in this construct is		
XX	comprised of 1010 bp of promoter and 170 bp of untranslated 5' leader		
XX	interrupted by a 1100 bp intron sequence		
XX			
XX	Sequence 9361 BP; 2449 A; 2285 C; 2190 G; 2435 T; 0 U; 2 Other;		
Query Match	97.2%; Score 2133.4; DB 3; Length 9361;		
Best Local Similarity	99.1%; Pred. No. 0;		
Matches 2167; Conservative	0; Mismatches 16; Indels 4; Gaps 2		

OY		10	AGTTTCGCACCGTTTTCACGCTCCTAACATAATAGGGAAGTGCTTAATATPAA	69
Dd		7083	AGTTCTCACCGTTTTTCACCCCCCTAACATAAATATGGGAAGCTGTCTAAATATPAA	7024
OY		70	ATGAGACTTATATATGTAGAGCGCTGATPACTAGAACCTATGTGAAGAAAACCTATCCACCCT	129
Dd		7023	ATGAGACTTATATATGTAGAGCGCTGATPACTAGAACCTATGTGAAGAAAACCTATCCACCCT	6964
OY		130	ACTTAGTGGCAATCGGGCTAAATATAAAAAGATGCGTACACTAGTTGCTTTTCCTTAG	189
Dd		6963	ACTTAGTGGCAATCGGGCTAAATATAAAAAGATGCGTACACTAGTTGCTTTTCCTTAG	6904
OY		190	TAAATTAGTGGGAAAAATGAATCATTTATGCTTAGAATATAAGTTCAATCTGTGCATG	249
Dd		6903	TAAATTAGTGGGAAAAATGAATCATTTATGCTTAGAATATAAGTTCAATCTGTGCATG	6844
OY		250	AAGTTAAATTATTCGAGGTAGCGCAATATTGTCATCAAACCTCTTCTGTAATAAAAAATCT	309
Dd		6843	AAGTTAAATTATTCGAGGTAGCGCAATATTGTCATCAAACCTCTTCTGTAATAAAAAATCT	6784
OY		310	TTCTAGCTGAACCTCAATGGGATTAAGAGAGATATTTTTTTTTAAAAAAAATAGATGAAG	369
Dd		6783	TTCTAGCTGAACCTCAATGGGATTAAGAGAGATATTTTTTTTT--AAAAAAAAATGATGAAG	6727
OY		370	ATATTCTGAACGTATACGGCAAAAGATTTTAAACATATATATATATATTTATAGTTGTGC	429
Dd		6726	ATATTCTGAACGTATATGGCAAAAGATTTTAAACATATATATATATATTTATAGTTGTGC	6667
OY		430	ATTGCTTATATCGACGTCATTTAAGGACATGTCCTTACCTCAATTTTATTTATAGTA	489
Dd		6666	ATTGCTCATATCGCACATCTTAAAGGACATGTCCTTACCTCAATTTTATTTATAGTA	6607
OY		490	ATTAAAGCAATPGACTATTTTTATTTATCTTTTTCGATTAGATGCAAGTACTT	549
Dd		6606	ATTAAAGCAATTTGACTTATTTTATTTATCTTTTTCGATTAGATGCAAGTACTT	6547
OY		550	ACGCACACACTTGTGTCTCATGTGCANTGTGATGACACTCTCTC-ATACACGTTCAACT	608
Dd		6546	AOCGACACACTTTGTGTCTCATGTGCANTGTGATGACACTCTCTCAATACACGTTCAACT	6487
OY		609	AGCGACACATCTCCAAATATCACTGCGCTATTTTATATCACTTAGTAGCAATATCTGAATT	668
Dd		6486	AGCAACACATCTCTAATATCACTGCGCTATTTTATATCACTTAGTAGCAATATCTGAATT	6427
OY		669	CAAGCACTTCAACCAATCAACACACCACTTTTAAATACTAATAATACAAAAATPATTTT	728
Dd		6426	CAAGCACTTCAACCAATCAACACCACTTTTAAATACTAATAATACAAAAATPATTTT	6367
OY		729	ACAGAATAGCANAAAAATATGAACGAACATATTAGTGTTTTCACATACAAAAAAA	788
Dd		6366	ACAAGATAGCATGAAAAATATGAACGAACATATTAGTGTTTTCACATACAAAAAAA	6307
OY		789	AGAAATTTTGCTGTGCGGAGCGCCAAATCTCCATATTGGGCAACAAGGCAACAAGAG	848
Dd		6306	AGAAATTTTGCTGTGCGGAGCGCCAAATCTCCATATTGGGCAACAAGGCAACAAGAG	6247
OY		849	TGCGTGCCTCCACAGAACCAACCAAAAAACGATGATCTAACAGAGGACACGAATGCCGA	908
Dd		6246	TGCGTGCCTCCACAGAACCAACCAAAAAACGATGATCTAACAGAGGACACGAATGCCGA	6187
OY		909	ACAACCTTTTAAACAGCAGGCTTTGGGCGAGAGAGAGAGAGAGGCAAGAAACCA	968
Dd		6186	ACAACCTTTTAAACAGCAGGCTTTGGGCGAGAGAGAGAGAGAGGCAAGAAACCA	6127
OY		969	GCAATCTCTCTCTCCCATCTATAAATTCTCCGCCCTTTTCCCTCTTATATAGAGGC	1028
Dd		6126	GCAATCTCTCTCTCCCATCTATAAATTCTCCGCCCTTTTCCCTCTTATATAGAGGC	6067
OY		1029	ATCCAAGCCAAAGAGGAGAGACCAAGACACGCACTTAGCAAGAAAGCCGACGACCG	1088
Dd		6066	ATCCAAGCCAAAGAGGAGAGACCAAGACACGCACTTAGCAAGAAAGCCGACGACCG	6007

QY	1089	CGTTCCTGCACCAATCTCCGGTCAGATCTGGTCGATCTCTCCCTCCACCTC	1148
Db	6006	CTCTTCCTGCACCAATCTCCGGTCAGATCTGGTCGATCTCTCCCTCCACCTC	5947
QY	1149	CTCTGCACAGGGATGTGCCTTCGGTGTCTTCGATTTATTTATGTTCTAGGTGTGAT	1208
Db	5946	CTCTGCACAGGGATGTGCCTTCGGTGTCTTCGATTTATTTATGTTCTAGGTGTGAT	5887
QY	1209	ACGGGCGTGAATGTTAGAAAAGGGGATCTGTATCTGTATGATATTCCTGTTCTTGGATTTG	1268
Db	5886	ACGGGCGTGAATGTTAGAAAAGGGGATCTGTATCTGTATGATATTCCTGTTCTTGGATTTG	5827
QY	1289	GGATTAAGAGGGGTTCTTGATGTTTGATGTGTATCCGTTTCGGTTTGAATTAGTATGTTTT	1328
Db	5826	GGATTAAGAGGGGTTCTTGATGTTTGAATGTGTATCCGTTTCGGTTTGAATTAGTATGTTTT	5767
QY	1329	CAATCGTCTGGAGAGCTCTATGAAATGAAATGTTTTAGGGTACGGAATCTTCGGATTTT	1388
Db	5766	CAATCGTCTGGAGAGCTCTATGAAATGAAATGTTTTAGGGTACGGAATCTTCGGATTTT	5707
QY	1389	GTGAGTACCTTTTGTGAGGTAAATCAGAGCACGGGTGATTTTGTGTGTATATAA	1448
Db	5706	GTGAGTACCTTTTGTGAGGTAAATCAGAGCACGGGTGATTTTGTGTGTATATAA	5647
QY	1449	AGTACATTTGTTTGGTCTCGATTCGTGTATGATGCTTCTCCATTTGACGAAGCTATCC	1508
Db	5646	AGTACCGTGTGTTGGTCTCTCGATTCGTGTATGATGCTTCTCCATTTGACGAAGCTATCC	5587
QY	1509	TTTGTTATTCCTCATTTGAACAAAATATCCAACTTTGAAAGAGGTCCTGTATGAGA	1568
Db	5586	TTTGTTATTCCTCATTTGAACAAAATATCCAACTTTGAAAGAGGTCCTGTATGAGA	5527
QY	1569	TTGATATGTTGATTTCTTAAGCTGTGCCAAATTTCCGACGTGCTGTGTTAGATACATA	1628
Db	5526	TTGATATGTTGATTTCTTAAGCTGTGCCAAATTTCCGACGTGCTGTGTTAGATACATA	5467
QY	1629	GTCCCATCACGAATTCATGAAAACGTTATATCTCAGGAAACAGGGATTCCTGT	1688
Db	5466	GTCCCATCACGAATTCATGAAAACGTTATATCTCAGGAAACAGGGATTCCTGT	5407
QY	1689	CTTCGATTTGCTTTAGTCCGAAATTTTTTCCCAAATATCTTAATAAGTCACTTCT	1748
Db	5406	CTTCGATTTGCTTTAGTCCGAAATTTTTTCCCAAATATCTTAATAAGTCACTTCT	5347
QY	1749	GGTTCAGTTCAGTAAATTTGCTTACAAATATATGCTTTTATAGCGTTATCTAGCTGTA	1808
Db	5346	GGTTCAGTTCAGTAAATTTGCTTACAAATATATGCTTTTATAGCGTTATCTAGCTGTA	5287
QY	1809	GTTTCAGTTTATAGGTAAATCCCTATATAGTTAGTCAGAGAGAACTTATCCGATTTCTG	1868
Db	5286	GTTTCAGTTTATAGGTAAATCCCTATATAGTTAGTCAGAGAGAACTTATCCGATTTCTG	5227
QY	1869	ATCTCCATTTTATATATATGAAATGAACTGTAGCAATAGCAGATTCATTTGGATATAT	1928
Db	5226	ATCTCCATTTTATATATATGAAATGAACTGTAGCAATAGCAGATTCATTTGGATATAT	5167
QY	1929	TTTTTTATAGCTTCAACCCCTCATTTATCTGAGCTGAAAGTCTGGCATGAATCTGTCT	1988
Db	5166	TTTTTTATAGCTTCAACCCCTCATTTATCTGAGCTGAAAGTCTGGCATGAATCTGTCT	5107
QY	1989	CAATTTTGTTTCAAAATTCACATGATTTATCTATGATATCTCTTGTATCTACCTGTA	2048
Db	5106	CAATTTTGTTTCAAAATTCACATGATTTATCTATGATATCTCTTGTATCTACCTGTA	5047
QY	2049	GAACTTTCCTTTTGGTATATCTCTGACTGCTGATTAACAGAAAGAAATTTATGAACTGT	2108
Db	5046	GAACTTTCCTTTTGGTATATCTCTGACTGCTGATTAACAGAAAGAAATTTATGAACTGT	4987
QY	2109	AATCGGGATGATTAATACGCTGTTCTTATGATTCATTTCTCTTGTGACAGTCTTGGTGT	2168
Db	4986	AATCGGGATGATTAATACGCTGTTCTTATGATTCATTTCTCTTGTGACAGTCTTGGTGT	4927
QY	2169	AGCTTGCCACTTTCACGACAAAGTTC	2195

|||||  
DB 4926 AGCTTGCCACTTTCACACGAAAGTTTC 4900  
RESULT 4  
AAD01286/c  
ID AAD01286 standard; DNA; 10629 BP.  
XX AAD01286;  
AC  
XX  
XX  
DT 12-OCT-2000 (first entry)  
DE Rice transformation vector, pARGOS2Af-hpt.  
XX  
XX Matrix Attachment Region; MAR; rice transformation vector; pARGOS2Af-hpt;  
KM scaffold attachment region; gene expression; transgenic organism; de.  
XX  
XX Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FH misc\_feature 2735..3389  
FT /tag= a  
FT /note= "Corresponds to nucleotides 14-668 of MAR dimer-2"  
FT misc\_feature 7730..8384  
FT /tag= b  
FT /note= "Corresponds to nucleotides 1-655 of MAR dimer-1"  
XX  
XX MO20032800-A1.  
XX  
XX 08-JUN-2000.  
XX  
XX 30-NOV-1999; 99WO-US028123.  
XX  
XX PR 01-DEC-1998; 98US-0110437P.  
XX  
XX (DMC ) DOW AGROSCIENCES LLC.  
XX  
XX Van Der Geest AHM, Ainley WM, Cowen NM, Welter ME, Woosley AT;  
XX  
XX WPI; 2000-412345/35.  
XX  
XX An isolated DNA molecule for use as a matrix attachment region to  
PT increase expression of genes introduced in transformed plants comprises a  
PT 298 base pair sequence described in the specification.  
XX  
XX  
XX PS Example 3; Page 51-54; 73pp; English.  
XX  
XX The patent discloses a DNA molecule, useful as matrix attachment region  
CC (MAR) or scaffold attachment region, to increase the expression of genes  
CC introduced in transformed plants. MARs are located in non-transcribed  
CC regions of genes and form the physical boundaries of individual DNA  
CC loops. They are rich in adenosine and thymine bases and contain certain  
CC conserved sequence elements and structural features. They are about 300-  
CC 2000 bp in length. Increased levels of expression of DNA introduced into  
CC plants can be achieved by use of MAR. They can also reduce the position  
CC effect in transgenic organisms. The present DNA sequence is the rice  
CC transformation vector pARGOS2Af-hpt, identical to the vector pGOS2-hpt,  
CC except that it contains a MAR dimer-2 positioned 5' to the GOS2  
CC transcription initiation region and the MAR dimer-1 positioned 3' to the  
CC nos 3' UTR (untranslated region). This vector is used to efficiently  
CC transform monocot plants like rice  
XX  
XX Sequence 10629 BP; 2904 A; 2469 C; 2369 G; 2887 T; 0 U; 0 Other;  
SQ  
Query Match 97.2%; Score 2133.4; DB 3; Length 10629;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 2167; Conservative 0; Mismatches 16; Indels 4; Gaps 2;  
QY 10 AGTTTCGACCGTTTTCACGTCCTAACAATATAGGAACGTGCTAAATATAA 69  
DB 7722 AGTTTCGACCGTTTTCACCGCTTAACAATATAGGAACGTGCTAAATATAA 7663  
QY 70 ATGAGACCTTATATATGTAAGCGCTGATAACTAGAACTATGTAAGAAAACTCATCCACT 129

|||||  
DB 7662 ATGAGACCTTATATATGTAAGCGCTGATAACTAGAACTATGCAAGAAAACTCATCCACT 7603  
QY 130 ACTTAGTGGAATCGGCTAAATTAATAAGATCGTACACTAGTTTCGTTTCTTAG 189  
DB 7602 ACTTAGTGGAATCGGCTAAATTAATAAGATCGTACACTAGTTTCGTTTCTTAG 7543  
QY 190 TAAATTAAGTGGAATAATGAATCATTAATGCTTGAATATAGTTTCACATCTGTCATG 249  
DB 7542 TAAATTAAGTGGAATAATGAATCATTAATGCTTGAATATAGTTTCACATCTGTCATG 7483  
QY 250 AAGTTAAATTAATGAGGTACCAATTAATGCACTAACTCTCTGTAATTAATAAATCT 309  
DB 7482 AAGTTAAATTAATGAGGTACCAATTAATGCACTAACTCTCTGTAATTAATAAATCT 7423  
QY 310 TTCTAGCTGAATCTAAATGGTAAAGAGATATTTTAAAAAATAAGATGAG 369  
DB 7422 TTCTAGCTGAATCTAAATGGTAAAGAGATATTTTAAAAAATAAGATGAG 7366  
QY 370 ATATTCTGAACGTAATCGGCAAGATTTAAACATATTAATTAATTAATTAATGTTGTGC 429  
DB 7365 ATATTCTGAACGTAATCGGCAAGATTTAAACATATTAATTAATTAATTAATGTTGTGC 7306  
QY 430 ATTGCTTATATCGACGCTATTAAGACATGCTTACCTCCATCTTCATTTTATTTAGTA 489  
DB 7305 ATTGCTTATATCGACGCTATTAAGACATGCTTACCTCCATCTTCATTTTATTTAGTA 7246  
QY 490 ATTAAGAACAATGACTATTTTATTTATTTATTTATCTTTTTCGATTAGTCAAGTACTT 549  
DB 7245 ATTAAGAACAATGACTATTTTATTTATTTATTTATTTTTCGATTAGTCAAGTACTT 7186  
QY 550 ACGCACACATTTGTGCTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 608  
DB 7185 ACGCACACATTTGTGCTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 7126  
QY 609 AGCGACATATCTCCAAATATGCACTGCGCTATTTATATGCTTATAGTACCAATATCTGAAT 668  
DB 7125 AGCAACACATCTCTAATATGCACTGCGCTATTTATATGCTTATAGTACCAATATCTGAAT 7066  
QY 669 CAAGCACTTTCACATATGCACTGCGCTATTTATATGCTTATAGTACCAATATCTGAAT 728  
DB 7065 CAAGCACTTTCACATATGCACTGCGCTATTTATATGCTTATAGTACCAATATCTGAAT 7006  
QY 729 ACAGATATGATGAATAAGATGAACGAATGATTTAGTTTTCACATCAATCAAAAAA 788  
DB 7005 ACAGATATGATGAATAAGATGAACGAATGATTTAGTTTTCACATCAATCAAAAAA 6946  
QY 789 AGAATTTTGTGCTGCGGCAAGCGCAATCTCCCATTTTGGGCAACAGGCAACCAAGAG 848  
DB 6945 AGAATTTTGTGCTGCGGCAAGCGCAATCTCCCATTTTGGGCAACAGGCAACCAAGAG 6886  
QY 849 TGGTGCACCAAGAACCAACCAAAAAACGATGATCTTAACGAGGACAGCAAGTCCGCA 908  
DB 6885 TGGTGCACCAAGAACCAACCAAAAAACGATGATCTTAACGAGGACAGCAAGTCCGCA 6826  
QY 909 ACAACCTTTTAAACAGACGCTTTCGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 968  
DB 6825 ACAACCTTTTAAACAGACGCTTTCGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6766  
QY 969 GCATCTCTCTCTCTCCCATCTTAATTAATTCCTCCCTTTTCCCTCTTAATTAAGAGGC 1028  
DB 6765 GCATCTCTCTCTCTCCCATCTTAATTAATTCCTCCCTTTTCCCTCTTAATTAAGAGGC 6706  
QY 1029 ATCCAGGCAAG 1088  
DB 6705 ATCCAGGCAAG 6646  
QY 1089 CTTTCTTCGATCATATCTTCGAGTTCGAGTTCTTGTGATCTCTTCCTTCACCTC 1148  
DB 6645 CTTTCTTCGATCATATCTTCGAGTTCGAGTTCTTGTGATCTCTTCCTTCACCTC 6586  
QY 1149 CTCCTCACAGGATATGTCCTTGGTTGTTTGGATTTATTTCTTCAAGTTTGTAGT 1208



D 6585 CTCTCAGCAGGATATGTCCTTGGTTGTTCTTGAATTAATGTTCTAGCTGTGACT 6526  
Q 1209 ACGGCGCTTGATGTTAGGAAAGGGAGCTGATCTGATGATGATGATCTTGGATTTG 1268  
D 6525 ACGGCGCTTGATGTTAGGAAAGGGAGCTGATCTGATGATGATGATCTTGGATTTG 6466  
Q 1269 GATATGAGGGGCTTCTGATGTTGATGATGATGATGATGATGATGATGATGATG 1328  
D 6465 GATATGAGGGGCTTCTGATGTTGATGATGATGATGATGATGATGATGATGATG 6406  
Q 1329 CAATCGCTGAGAGCTCTATGAGAAATGATGATGATGATGATGATGATGATGATGAT 1388  
D 6405 CAATCGCTGAGAGCTCTATGAGAAATGATGATGATGATGATGATGATGATGATGAT 6346  
Q 1389 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1448  
D 6345 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6286  
Q 1449 AGTACATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1508  
D 6285 AGTACATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 6226  
Q 1509 TTTGTTATTCCTCATTTGAAAGAAATATCAACTTGAAGACGGCTGTTGATGAGA 1568  
D 6225 TTTGTTATTCCTCATTTGAAAGAAATATCAACTTGAAGACGGCTGTTGATGAGA 6166  
Q 1569 TTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1628  
D 6165 TTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6106  
Q 1629 GTCCCATGACGAAATTCATGAAACAGTTATATCTCAGAAACAGGGGATTCCTGTT 1688  
D 6105 GTCCCATGACGAAATTCATGAAACAGTTATATCTCAGAAACAGGGGATTCCTGTT 6046  
Q 1689 CTTCAGATTTGCTTTAGTCCGAGAAATTTTTCGAGAAATCTTAAAGTCACTTCT 1748  
D 6045 CTTCAGATTTGCTTTAGTCCGAGAAATTTTTCGAGAAATCTTAAAGTCACTTCT 5986  
Q 1749 GGTTCAGTTCATGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1808  
D 5985 GGTTCAGTTCATGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 5926  
Q 1809 GTTCAGTTATAGGATATATCCCTATAGTTAGTCAGAGAAAGTATTCGATTTCTG 1868  
D 5925 GTTCAGTTATAGGATATATCCCTATAGTTAGTCAGAGAAAGTATTCGATTTCTG 5866  
Q 1869 ATCTCAATTTTATATATGAAATGAACTGATGATGATGATGATGATGATGATGAT 1928  
D 5865 ATCTCAATTTTATATATGAAATGAACTGATGATGATGATGATGATGATGATGAT 5806  
Q 1929 TTTTATATAGCTTCAACCTTCATTAATCTGAGCTGAAGCTGGCATGATGCTGCT 1988  
D 5805 TTTTATATAGCTTCAACCTTCATTAATCTGAGCTGAAGCTGGCATGATGCTGCT 5746  
Q 1989 CAATTTGTTTCAAAATTCATGATGATGATGATGATGATGATGATGATGATGATG 2048  
D 5745 CAATTTGTTTCAAAATTCATGATGATGATGATGATGATGATGATGATGATGATG 5686  
Q 2049 GAAATTTCTTTTGGTTATCTGTAAGCTGTTGATGATGATGATGATGATGATGAT 2108  
D 5685 GAAATTTCTTTTGGTTATCTGTAAGCTGTTGATGATGATGATGATGATGATGAT 5626  
Q 2109 AATCGGATAGTATATCTGCTGTTGATGATGATGATGATGATGATGATGATGATG 2168  
D 5625 AATCGGATAGTATATCTGCTGTTGATGATGATGATGATGATGATGATGATGATG 5566  
Q 2169 AGCTTGCACTTTACACAGCAAGTTC 2195  
D 5565 AGCTTGCACTTTACACAGCAAGTTC 5539

RESULT 5  
ADY69039

ID ADY69039 standard; DNA; 2191 BP.  
AC ADY69039;  
XX  
XX  
DT 02-JUN-2005 (first entry)  
XX  
XX GOS2 promoter DNA.  
XX  
XX plant; crop improvement; B-type cyclin dependent kinase; CDK; de;  
KM promoter; GOS2.  
OS unidentified.  
PN WO2005024029-A2.  
XX  
XX 17-MAR-2005.  
PD  
XX  
PF 03-SEP-2004; 2004WO-BE052035.  
PR  
XX 05-SEP-2003; 2003EP-00077811.  
XX  
XX (CROP-) CROPDESIGN NV.  
PA  
PI Broekaert W, Frankard V, Hatzfeld Y, Mironov V;  
XX  
XX MPI; 2005-223384/23.  
DR  
XX  
PT Improving plant growth characteristics, e.g. increased yield, increased  
XX growth rate, or modified architecture, comprises increasing expression in  
XX a plant of a nucleic acid encoding a B-type cyclin dependent kinase (CDK)  
XX protein and/or increasing activity and/or levels in a plant of a B-type  
XX CDK protein. INDEPENDENT CLAIMS are also included for: plants obtained  
XX using the method above; construct comprising (i) a B-type CDK  
XX gene/nucleic acid encoding a B-type CDK protein, or (ii) a nucleic acid  
XX encoding a CDK mutant, which CDK mutant comprises at least one of the 7  
XX amino acid position changes or at least one of the 8 amino acid position  
XX changes listed in the disclosure, (iii) one or more control sequences  
XX capable of driving expression of the nucleic acid of (i) or (ii), and  
XX optionally (iv) a transcription termination sequence; a method for  
XX producing transgenic plant having improved growth characteristics, e.g.  
XX increased yield, increased growth rate, or modified architecture, which  
XX growth characteristics are improved relative to growth characteristics of  
XX corresponding wild type plants; transgenic plant having improved growth  
XX characteristics, e.g. increased yield, increased growth rate, or modified  
XX architecture, the plant has increased expression of a B-type CDK nucleic  
XX acid and/or increased activity and/or levels in a plant of a B-type CDK  
XX protein relative to corresponding wild type plants; a composition  
XX comprising a protein comprising a sequence of 309, 311, or 315 amino  
XX acids (SEVEN SEQ ID NOS: 2-6), or its homologue, derivative, or active  
XX fragment, used as a growth regulator; a screening method for identifying  
XX mutant plant CDKs having enhanced CDK activity relative to corresponding  
XX non-mutant plant CDKs; a screening method for identifying substantially  
XX non-active plant CDKs, but are capable of binding to plant CKs; mutant  
XX CDKs obtained using the methods of (6) and (7), where the mutants bind to  
XX cyclin but not to CK as listed in the disclosure, or where the mutants  
XX bind to CK but not to cyclin as listed in the disclosure; an isolated  
XX nucleic acid molecule comprising (i) a nucleic acid encoding a CDK mutant  
XX comprising any of the 5 sequences of 294 amino acids each (SEQ ID NOS: 9-  
XX 13), or (ii) a nucleic acid molecule encoding a homologue, derivative,  
XX or active fragment of a CDK mutant of SEQ ID NOS: 9-11, where the homologue,  
XX derivative or active fragment comprised at least one of the 7 amino acid  
XX position changes or at least one of the 8 amino acid position changes  
XX listed in the disclosure, (iii) a nucleic acid capable of hybridizing  
XX with a nucleic acid of (i) or (ii), where the hybridizing sequence  
XX encodes an amino acid comprising at least one of the 7 amino acid  
XX position changes or at least one of the 8 amino acid position changes  
XX listed in the disclosure, (iv) a nucleic acid of (i) to (iii) which is



degenerate as a result of the genetic code, (v) allelic variants of (i) to (iv), where the allelic variant encodes an amino acid comprising at least one of the 7 amino acid position changes or at least one of the 8 amino acid position changes listed in the disclosure, or (vi) alternative splice variants of nucleic acids of (i) to (v), where the alternative splice variants encodes an amino acid comprising at least one of the 7 amino acid position changes or at least one of the 8 amino acid position changes listed in the disclosure, and a CDK mutant comprising (i) an amino acid sequence of SEQ ID NOS: 9-13, or (ii) a fragment of SEQ ID NOS: 9-13 where the fragment comprises at least one of the 7 amino acid position changes or at least one of the 8 amino acid position changes listed in the disclosure. Preferred Method: Increasing expression is effected by introducing and expressing in a plant a B-type CDK nucleic acid. The B-type CDK is derived from a plant, algal, or fungal source. The B-type CDK derived from a plant is from a dicotyledonous plant, preferably from the family Brassicaceae, specifically Arabidopsis thaliana. The B-type CDK is a class 1 B-type CDK, preferably a CDK B1,1 or CDK B1,2 from A. thaliana. The B-type CDK is a class 2 B-type CDK, preferably a CDK B2,2 from A. thaliana. The CDK B1,1 nucleic acid comprises a sequence of 930 bp (SEQ ID NO: 1), or its portion, or a nucleic acid capable of hybridizing to SEQ ID NO: 1, and where the CDK B1,1 protein comprises a sequence of SEQ ID NO: 2 or its homologue, derivative or active fragment. The CDK B1,1 nucleic acid comprises a sequence of 936 bp (SEQ ID NO: 3), or its portion, or a nucleic acid capable of hybridizing to SEQ ID NO: 3, and where the CDK B1,2 protein comprises a sequence of SEQ ID NO: 4 or its homologue, derivative or active fragment. The CDK B2,2 nucleic acid comprises a sequence of 948 bp (SEQ ID NO: 5), or its portion, or a nucleic acid capable of hybridizing to SEQ ID NO: 5, and where the CDK B2,2 protein comprises a sequence of SEQ ID NO: 6 or its homologue, derivative or active fragment. The B-type CDK is a variant nucleic acid or variant amino acid, e.g. functional portions of, sequences capable of hybridizing to, alternative splice variants of, or allelic variants of a B-type CDK nucleic acid/gene, homologues, derivatives, or active fragments of a B-type CDK protein, or mutant B-type CDKs. The expression of the CDK B1,1 nucleic acid is driven by a promoter active in young, expanding tissue, preferably where the promoter is beta expansin promoter. The expression of CDK B1,2 nucleic acid CDK B2,2 nucleic acid is driven by a constitutive promoter, specifically a GGS 2 promoter. The increased yield comprises increase in area, increase in the number of particles, increased in height, increase in the number of seeds, increase in the number of filled seed, increase in total weight of seeds, increase in thousand kernel weight (TKW), or an increase in harvest index, each relative to control plants. The modified architecture includes increase in aboveground area, increase in the number of particles or increase in height. Producing transgenic plant having improved growth characteristics, e.g. increased yield, increased growth rate, or modified architecture, which growth characteristics are improved relative to growth characteristics of corresponding wild type plants, comprises introducing into a plant or a plant cell a B-type CDK gene/nucleic, or a nucleic acid encoding a CDK mutant comprising at least one of the 7 amino acid position changes listed in the disclosure, and culturing the plant cell under conditions promoting regeneration and mature plant growth. Identifying mutant plant CDKs having enhanced CDK activity relative to corresponding non-mutated plant CDKs comprises providing plant-derived CDK mutants, identifying cyclin dependent kinase inhibitor (ICK) non reacting mutants, identifying mutants having cyclin-binding activity, and optionally a yeast complementation assay on resultant mutants. Identifying substantially non-active plant CDKs, but are capable of binding to plant ICKs, comprises providing plant-derived CDK mutants, identifying plant-ICKs, which growth characteristics are identifying non-cyclin binding mutants. The CDK mutants are provided by providing a wild type plant CDK and mutating the CDK at least 1 amino acid position. Preferred Transgenic Plant: The plant is a monocotyledonous plant. The CDK B-type nucleic or CDK B-type amino acid is useful for improving the growth characteristics of a plant, the growth characteristics is increased yield, increased growth rate, or modified architecture (claimed).

Sequence 2191 BP; 638 A; 431 C; 403 G; 719 T; 0 U; 0 Other;

Query Match	96.4%	Score 2115.2	DB 14	Length 2191
Best Local Similarity	98.9%	Pred. No. 0		
Matches 2172; Conservative	0	Mismatches 18	Indels 6	Gaps 4

QY	1	AATCGAAAACATTTCTGACACGGTTTTCAGCTGCTACCTAAACAATATGAGGAAACGTGCT	60
Db	1	AATCGAAAACATTTCTGACACGGTTTTCAGCTGCTACCTAAACAATATGAGGAAACGTGCT	60
QY	61	AAATATATAAATAGAACCTTATATATATGATGCGCTGATTAATCTGAACTATGTAAGAAAACT	120
Db	61	AAATATATAAATAGAACCTTATATATATGATGCGCTGATTAATCTGAACTATGTAAGAAAACT	120
QY	121	CATCCACTCTTATAGTGGCAATGGGGCTAAATTAATAAAGTGGCTTACACTAGTTTGGT	180
Db	121	CATCCACTCTTATAGTGGCAATGGGGCTAAATTAATAAAGTGGCTTACACTAGTTTGGT	180
QY	181	TTTCCCTTAGTAATTAAGTGGGAAAAATGAAATCATTTATGCTTAGAATATAGCTTACATC	240
Db	181	TTTCCCTTAGTAATTAAGTGGGAAAAATGAAATCATTTATGCTTAGAATATAGCTTACATC	240
QY	241	TCTGTCATGAAGTTAAATTAATTCGAGGTAGCCATPATTTGTCATCAAACTCTTCTGTAATA	300
Db	241	TCTGTCATGAAGTTAAATTAATTCGAGGTAGCCATPATTTGTCATCAAACTCTTCTGTAATA	300
QY	301	AAAAAATCTTTCTAGCTGTAATCTCAATGGGTAAAGAGATATTTTTTTTTTAAAAAAT	360
Db	301	AAAAAATCTTTCTAGCTGTAATCTCAATGGGTAAAGAGATATTTTTTTTTTAAAAAAT	360
QY	361	AGAAATGAAGATATTCTGAAACGTATTCGGCAAGATTTAAACATATATATATTAATTTTAT	420
Db	358	AGAAATGAAGATATTCTGAAACGTATTCGGCAAGATTTAAACATATATATTAATTTTAT	417
QY	421	AGTTTGTGCATCGTTATATGCAACGTCTTAATAGGACATGCTCTTACCTCATCTCATTTT	480
Db	418	AGTTTGTGCATCGTCTATATGCAACATCTTAATAGGACATGCTCTTACCTCAACCTCAATTTT	477
QY	481	TATTTAGTAATTAAGAACAATTGACTTATTTTATTTTATTTTATCTTTTTCGATTAGATGC	540
Db	478	TATTTAGTAATTAAGAACAATTGACTTATTTTATTTTATTTTATCTTTTTCGATTAGATGC	537
QY	541	AAGGTACTTACGACACACTTTGTGCTCATGTGTCATGTGTGATGTCACCTCTC - ATPACA	599
Db	538	AAGGTACTTACGACACACTTTGTGCTCATGTGTCATGTGTGATGTCACCTCTCMAATGACA	597
QY	600	CGTTCAACTAGCGACACATCTCCAAATATCACTCGCCATTTTAATACATTTAGGTAGCAAT	659
Db	598	CGTTCAACTAGCGACACATCTCTTAATATCACTCGCCATTTTAATACATTTAGGTAGCAAT	657
QY	660	ATCTGAATTCAGAGACTTCACCATCACGACACACTTTTAAATATCTAATAATACAAATA	719
Db	658	ATCTGAATTCAGAGACTTCACCATCACGACACACTTTTAAATATCTAATAATATACAAATA	717
QY	720	AATATATTTTACAGAAATAGCATGAAAGATATGAAACGAATATTTTAGTTTTCACATPACA	779
Db	718	AATATATTTTACAGAAATAGCATGAAAGATATGAAACGAATATTTTAGTTTTCACATPACA	777
QY	780	AAAAAATAAATATTTTGTGCTGTGCGGAGGCGCAATCTCCCATATTTGGGACACACGACA	839
Db	778	AAAAAATAAATATTTTGTGCTGTGCGGAGGCGCAATCTCCCATATTTGGGACACACGACA	837
QY	840	ACAAACAGAGTGGCTGCCACAGAAACAACCCACAATAAAGATATCTTAACGAGAGACAGC	899
Db	838	ACAAACAGAGTGGCTGCCACAGAAACAACCCACAATAAAGATATCTTAACGAGAGACAGC	897
QY	900	AAGTCCGCAACAACCTTTTAAACACAGGCTTTGGCGCCAGGAGAGAGAGAGAGGACAA	959
Db	898	AAGTCCGCAACAACCTTTTAAACACAGGCTTTGGCGCCAGGAGAGAGAGAGAGGACAA	957
QY	960	GAATAACCAAGATCTCTCTCTCCCATCTAATAATTTCTCCGCCCTTTTCCCTCTCTAT	1019
Db	958	GAATAACCAAGATCTCTCTCTCCCATCTAATAATTTCTCCGCCCTTTTCCCTCTCTAT	1017
QY	1020	ATPAGAGGCATCCAAAGCCAAAGAGAGGAGAGACCAAGACACGCGCATATGCAAGAGCC	1079
Db	1018	ATPAGAGGCATCCAAAGCCAAAGAGAGGAGAGACCAAGAGACACGCGCATATGCAAGAGCC	1077

QY 1080 GAGCGACCGCTCTTCGATCCATATCTTCCGGTCGAGTTCTTGCTGATCTCTCCCTC 1139  
DB 1078 GAGCGACCGCTCTTCGATCCATATCTTCCGGTCGAGTTCTTGCTGATCTCTCCCTC 1137  
QY 1140 CTCACCTCTCTCTCAAGGATATGCCCCCTCGGTTGTTCTTGATTTATGTTCTTAG 1199  
DB 1138 CTCACCTCTCTCTCAAGGATATGCCCCCTCGGTTGTTCTTGATTTATGTTCTTAG 1197  
QY 1200 TTGTGATGACGGGCGTTGATGTTAGAAAGGGATCTGTATCTGATGATCTCTGTC 1259  
DB 1198 TTGTGATGACGGGCGTTGATGTTAGAAAGGGATCTGTATCTGATGATCTCTGTC 1257  
QY 1260 TTGTGATGAGATAGAGGGGTTCTGTATGTTGATGTTATCGGTTGCTTGAATTAG 1319  
DB 1258 TTGTGATGAGATAGAGGGGTTCTGTATGTTGATGTTATCGGTTGCTTGAATTAG 1317  
QY 1320 TATGTTTTCATCGTCTGAGAGCTCTATGGAATGAAATGTTTATGAGTACGGAATCT 1379  
DB 1318 TATGTTTTCATCGTCTGAGAGCTCTATGGAATGAAATGTTTATGAGTACGGAATCT 1377  
QY 1380 TCGGATTTTGTAGTACCTTTTGTGAGGTAAATCAGAGCAGCGGTGATTTGCTTG 1439  
DB 1378 TCGGATTTTGTGA-TACCTTTTGTGAGGTAAATCAGAGCAGCGGTGATTTGCTTG 1436  
QY 1440 TGTATATATAAGTACATTTTGTGCTCTGATTCGTGATGATGCTTCTCGATTTGAG 1499  
DB 1437 TGTATATATAAGTACGTTTGTGCTCTGATTCGTGATGATGCTTCTCGATTTGAG 1496  
QY 1500 AAGCTATCTTGTGTTATTCCTATTTGAAACAAATATATCCAACTTTGAGAGCGTCCG 1559  
DB 1497 AAGCTATCTTGTGTTATTCCTATTTGAAACAAATATATCCAACTTTGAGAGCGTCCG 1556  
QY 1560 TTGATGAGATGATGATGATTTCTTAAAGCTGTCGAAATTTGCGAGCGGCTTGTTA 1619  
DB 1557 TTGATGAGATGATGATGATTTCTTAAAGCTGTCGAAATTTGCGAGCGGCTTGTTA 1616  
QY 1620 GATACAGTATGCTCCCATCAAGAAATCATGAAACAGTTATATCTTCAGAAACAGGGA 1679  
DB 1617 GATACAGTATGCTCCCATCAAGAAATCATGAAACAGTTATATCTTCAGAAACAGGGA 1676  
QY 1680 TTCCCTGTTCTTCGATTTGCTTAACTCCAGAAATTTTTCCTCAATATCTTAAAG 1739  
DB 1677 TTCCCTGTTCTTCGATTTGCTTAACTCCAGAAATTTTTCCTCAATATCTTAAAG 1736  
QY 1740 TCACCTTTCGTTCACTTCAAGAAATGATGTAATGCTTAAATGCTTATAGCTTATC 1799  
DB 1737 TCACCTTTCGTTCACTTCAAGAAATGATGTAATGCTTAAATGCTTATAGCTTATC 1796  
QY 1800 CTAGCTGATGTTCACTTCAAGAAATGCTTAACTCCATAGTTAGTCAGAGAAAGAACTTATC 1859  
DB 1797 CTAGCTGATGTTCACTTCAAGAAATGCTTAACTCCATAGTTAGTCAGAGAAAGAACTTATC 1856  
QY 1860 CGATTTCTGATCTCAATTTTAAATTAATGAAATGAACTGATGATGATGATGATTCAT 1919  
DB 1857 CGATTTCTGATCTCAATTTTAAATTAATGAAATGAACTGATGATGATGATGATTCAT 1916  
QY 1920 TGGATTTATTTTATTTATAGCTTCAAGCTTCAATTTCTGAGCTGGAAGCTGCGAG 1979  
DB 1917 TGGATTTATTTTATTTTATAGCTTCAAGCTTCAATTTCTGAGCTGGAAGCTGCGAG 1975  
QY 1980 AACTGCTCAATTTTATTTTCAAAATTCATGATGATTCATGATTCCTCTGAT 2039  
DB 1976 AACTGCTCAATTTTATTTTCAAAATTCATGATGATTCATGATTCCTCTGAT 2035  
QY 2040 CTACCTGATGATTTTATTTTGTGTTATCTTGAATGATTCAGAAAGAAATTTA 2099  
DB 2036 CTACCTGATGATTTTATTTTGTGTTATCTTGAATGATTCAGAAAGAAATTTA 2095  
QY 2100 TGAAGCTGATTCGAGATGATTAATGATGATTCATGATTCCTTGTGAGT 2159  
DB 2096 TGAAGCTGATTCGAGATGATTAATGATGATTCATGATTCCTTGTGAGT 2155  
QY 2160 TCTTGATGATTCGACATTTTCAAGAAAGTTTC 2195

DB 2156 TCTTGATGATTCGACATTTTCAAGAAAGTTTC 2191  
RESULT 5  
AAC88400  
ID AAC88400 standard; DNA; 898 BP.  
XX AAC88400;  
AC AAC88400;  
XX  
DT 02-MAR-2001 (first entry)  
XX  
XX Rice GOS2 enhancer.  
DE  
XX  
KM Glyphosate; 5-enolpyruvylshikimate phosphate synthase; EPSPS;  
KM herbicide resistance; se.  
XX  
OS Oryza sativa.  
XX  
PN WO20066746-A1.  
PN  
PD 09-NOV-2000.  
XX  
XX 20-APR-2000; 200WO-GB001559.  
PF  
XX 29-APR-1999; 99GB-00009971.  
PR 29-APR-1999; 99GB-00009972.  
PR 29-JUL-1999; 99GB-00017837.  
PR 29-JUL-1999; 99GB-00017842.  
PR 21-DEC-1999; 99GB-00030190.  
PR 21-DEC-1999; 99GB-00030206.  
PR 21-DEC-1999; 99GB-00030214.  
PR 21-DEC-1999; 99GB-00030216.  
XX  
XX (ZENBE ) ZENECA LTD.  
PA  
XX Hawkes TR, Warner SMJ, Andrews CJ, Bachoo S, Pickerrill AP;  
PI WPI; 2000-679763/66.  
XX  
DR  
XX  
PT Novel polynucleotide encoding the rice 5-enolpyruvylshikimate phosphate  
synthase, used to produce glyphosate tolerant or resistant plants.  
XX  
PS  
XX Disclosure; Page 55; 85pp; English.  
XX  
CC The present invention relates to a glyphosate resistant rice 5-  
enolpyruvylshikimate phosphate synthase (EPSPS) gene. This gene can be  
used to produce plant tissue and/or morphologically normal fertile whole  
CC plants which are tolerant or resistant to glyphosate herbicide, and in  
the production of a herbicidal target for the high throughput in vitro  
screening of potential herbicides  
XX  
SQ Sequence 898 BP; 320 A; 166 C; 137 G; 275 T; 0 U; 0 Other:  
Query Match 39.5%; Score 867.2; DB 3; Length 898;  
Best Local Similarity 99.2%; Pred. No. 7.4e-184;  
Matches 893; Conservative 0; Mismatches 3; Indels 4; Gaps 2;  
QY 1 AATCGAAAGTTTTCGACCGTTTTCAGCTCTTCACTTACATATATAGGAAAGCTGCT 60  
DB 2 AATCGAAAGTTTTCGACCGTTTTCAGCTCTTCACTTACATATATAGGAAAGCTGCT 61  
QY 61 AATATATAATGAGACCTTATATATGAGCGGTGATTAAGTAACTGATGATGATGATGAT 120  
DB 62 AATATATAATGAGACCTTATATATGAGCGGTGATTAAGTAACTGATGATGATGATGAT 121  
QY 121 CATCCACCTACTTATGATGATCGGCTTAAATATAAGAGTCCCTACACTAGTTTGT 180  
DB 122 CATCCACCTACTTATGATGATCGGCTTAAATATAAGAGTCCCTACACTAGTTTGT 181  
QY 181 TTTCTTATGATTAATGATGAGGAAATGAAATCATTTGCTTGAATATATGATGATGATC 240  
DB 182 TTTCTTATGATTAATGATGAGGAAATGAAATCATTTGCTTGAATATATGATGATGATC 241

QY 241 TCTGTCATGAGTAAATTATTGAGGTAGCCATAATTGTCATCAAACTCTTCTGGAATA 300  
DB 242 TCTGTCATGAGTAAATTATTGAGGTAGCCATAATTGTCATCAAACTCTTCTGGAATA 301  
QY 301 AAAAAATCTTTTCTAGCTGACATCAATGGGTAAAGAGAGATTTTTTTTTTAAAAAAT 360  
DB 302 AAAAAATCTTTTCTAGCTGACATCAATGGGTAAAGAGAGATTTTTTTTTTAAAAAAT 358  
QY 361 AGAATGAGATATATCTGAACTGATCGGCAAGATTTAAACATATATATATATATATAT 420  
DB 369 AGAATGAGATATATCTGAACTGATCGGCAAGATTTAAACATATATATATATATATAT 418  
QY 421 AGTTTGTCATTCGTTATATCGCAGCTCATTAAGAAGATGCTTCACTCATCTCAATTTT 480  
DB 419 AGTTTGTCATTCGTTATATCGCAGCTCATTAAGAAGATGCTTCACTCATCTCAATTTT 478  
QY 481 TATTTAGTAAATTAAGACATTTGACTTATTTTATTTATTTTATCTTTTTCGATTAGATCC 540  
DB 479 TATTTAGTAAATTAAGACATTTGACTTATTTTATTTATTTTATCTTTTTCGATTAGATCC 538  
QY 541 AAGGTACTTAGGCAACACTTTTGCTGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 599  
DB 539 AAGGTACTTAGGCAACACTTTTGCTGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 598  
QY 600 CGTTCACTAGGCAACACTTTTGCTGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 659  
DB 599 CGTTCACTAGGCAACACTTTTGCTGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 658  
QY 660 ATCTGAATTCAGACACTTCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 719  
DB 659 ATCTGAATTCAGACACTTCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 718  
QY 720 AATTAATTTTACGAAATAGCATGAAAGTATGAAACGAACTATTTAGTTTTCACATACA 779  
DB 719 AATTAATTTTACGAAATAGCATGAAAGTATGAAACGAACTATTTAGTTTTCACATACA 778  
QY 780 AAAAAAAGAAATTTTGTCTGTCGCGCAGCCCAATCTCCATATTTGGGCAACAGGCA 839  
DB 779 AAAAAAAGAAATTTTGTCTGTCGCGCAGCCCAATCTCCATATTTGGGCAACAGGCA 838  
QY 840 ACAACAGAGTGGCTGCCACAGAACACCCACAAAAAGATGATCTAACGAGAGACAGC 899  
DB 839 ACAACAGAGTGGCTGCCACAGAACACCCACAAAAAGATGATCTAACGAGAGACAGC 898

RESULT 7  
AAC87195  
ID AAC87195 standard; DNA, 898 BP.

XX AAC87195;  
XX  
DT 09-MAR-2001 (first entry)  
XX  
DE Rice GOS2 promoter enhancer element, SEQ ID NO:50.  
XX  
KW Rice EPSPS; 5-enolpyruvylshikimate phosphate synthase;  
KW glyphosate resistance; herbicide resistance; transgenic plant;  
KW expression construct; enhancer element; ds.  
XX  
OS Oryza sativa.  
XX  
PN MO20066748-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-GB001573.  
XX  
PR 29-APR-1999; 99GB-00009968.  
PR 29-JUL-1999; 99GB-00017834.  
PR 29-JUL-1999; 99GB-00017835.  
PR 29-JUL-1999; 99GB-00017840.  
PR 29-JUL-1999; 99GB-00017846.

PR 29-JUL-1999; 99GB-00017847.  
PR 21-DEC-1999; 99GB-00030200.  
PR 21-DEC-1999; 99GB-00030204.  
PR 21-DEC-1999; 99GB-00030207.  
PR 21-DEC-1999; 99GB-00030209.  
PR 21-DEC-1999; 99GB-00030213.  
XX  
PA (ZENEC) LTD.  
PI Hawkes TR, Warner SAJ, Andrews CJ, Bachoo S, Pickering AP;  
DR WPI: 2000-687544/67.  
XX  
XX  
PT Novel polynucleotide encoding 5-enolpyruvylshikimate phosphate synthase,  
PT having resistance or tolerance to glyphosate herbicide.  
XX  
PS Claim 18; Page 56; 87pp; English.  
XX  
XX The invention relates to rice 5-enolpyruvylshikimate phosphate synthase  
CC (EPSPS) genomic DNA (AAC87188). The invention also relates to an  
CC expression cassette comprising, in the 5'-3' direction, one or more  
CC transcriptional enhancer elements selected from AAC87190-C87196), the  
CC rice EPSPS promoter, genomic DNA encoding a rice EPSPS chloroplast  
CC transit peptide, genomic DNA encoding a EPSPS protein modified such that  
CC it is resistant to glyphosate (AAC87189), and a transcriptional  
CC terminator. The glyphosate resistant EPSPS contains a region (AAB29793)  
CC containing two amino acid substitutions relative to the corresponding  
CC wild-type region (AAB29792). The invention also encompasses plant genomic  
CC EPSPS sequences identified via screening with a rice EPSPS intronic  
CC sequence; vectors and host plant cells comprising a nucleic acid sequence  
CC of the invention; transgenic plants (and tissues and seeds thereof)  
CC comprising a nucleic acid sequence of the invention, optionally further  
CC transformed with a DNA encoding an insect, fungal, viral, bacterial,  
CC nematode, stress or herbicide resistance protein; and methods of  
CC producing the transgenic plants of the invention. The nucleic acids and  
CC constructs of the invention are used to produce a wide variety of  
CC morphologically normal, glyphosate resistant plants. The glyphosate  
CC resistant plants produced are particularly maize, soybean, cotton,  
CC sugarcane and canola, but also other field crops, fruits and vegetables,  
CC turf and forage grasses and nut-producing plants. The plants are  
CC optionally resistant to insects, fungi, viruses, bacteria, nematodes,  
CC stress, desiccation and/or other herbicides. They can be used in the  
CC production of a herbicidal target for the high throughput in vitro  
CC screening of potential herbicides. The present sequence represents an  
CC enhancer element which may be used in the rice EPSPS expression cassette  
CC of the invention  
XX  
SQ Sequence 898 BP; 320 A; 166 C; 137 G; 275 T; 0 U; 0 Other;  
XX  
Query Match 39.5%; Score 867.2; DB 3; Length 898;  
Best Local Similarity 99.2%; Pred. No. 7,4e-184;  
Matches 893; Conservative 0; Mismatches 3; Indels 4; Gaps 2;  
QY 1 AATCGAAAAGTTTCTGACCGTTTTCAGTCTTCACTTAACAATATAGGAACTGTCT 60  
DB 2 AATCGAAAAGTTTCTGACCGTTTTCAGTCTTCACTTAACAATATAGGAACTGTCT 61  
QY 61 AATATTAATAAGAGCCTTATATATATATATATATATATATATATATATATATATAT 120  
DB 62 AATATTAATAAGAGCCTTATATATATATATATATATATATATATATATATATATAT 121  
QY 121 CATCACCTACTTTAGTGGCAATCGGCTAATATATATATATATATATATATATATATAT 180  
DB 122 CATCACCTACTTTAGTGGCAATCGGCTAATATATATATATATATATATATATATATAT 181  
QY 181 TTTCTTATGTAATTAAGTGGGAAATGAATCATTTATTTGTTAGATATATACCTTCACTC 240  
DB 182 TTTCTTATGTAATTAAGTGGGAAATGAATCATTTATTTGTTAGATATATACCTTCACTC 241  
QY 241 TCTGTCATGAGTAAATTATTGAGGTAGCCATAATTGTCATCAAACTCTTCTGGAATA 300  
DB 242 TCTGTCATGAGTAAATTATTGAGGTAGCCATAATTGTCATCAAACTCTTCTGGAATA 301

QY 301 AAAAAATCTTTAGCTGAATCAATGCTGTAAGAGATATTTTTTTTAAAAAAAT 360  
 |||||  
 DB 302 AAAAAATCTTTAGCTGAATCAATGCTGTAAGAGATATTTTTTTT---AAAAAAT 358  
 |||||  
 QY 361 AGAATGAAGATATTCGAACGTAATCGCAAAAGATTAAATATATATATATATAT 420  
 |||||  
 DB 359 AGAATGAAGATATTCGAACGTAATCGCAAAAGATTAAATATATATATATATAT 418  
 |||||  
 QY 421 AGTTTGATGCTGTTATATGACGCTAATTAAGACATGCTACTCCATCTCAATTT 480  
 |||||  
 DB 419 AGTTTGATGCTGTTATATGACGCTAATTAAGACATGCTACTCCATCTCAATTT 478  
 |||||  
 QY 481 TATTTAGTATTAAGAATGATGATATTTATTTATTTATTTATTTTTCGATTAGATG 540  
 |||||  
 DB 479 TATTTAGTATTAAGAATGATGATATTTATTTATTTATTTATTTTTCGATTAGATG 538  
 |||||  
 QY 541 AAGGTACTTAAGCAACACTTTGCTCATGTCATGTCATGTCATGTCATGTCATGTC 599  
 |||||  
 DB 539 AAGGTACTTAAGCAACACTTTGCTCATGTCATGTCATGTCATGTCATGTCATGTC 598  
 |||||  
 QY 600 CGTTCACTAGGCAACATCTCAATATCACTGCTATTTATTAATAGATTAGTACAT 659  
 |||||  
 DB 599 CGTTCACTAGGCAACATCTCAATATCACTGCTATTTATTAATAGATTAGTACAT 658  
 |||||  
 QY 660 ATCTGAATTCAGACATCTCAACATCAACAGACCACTTTTAAATATCTAAATACAAA 719  
 |||||  
 DB 659 ATCTGAATTCAGACATCTCAACATCAACAGACCACTTTTAAATATCTAAATACAAA 718  
 |||||  
 QY 720 AATTAATTTTACAGATATGATGAAAAGTATGAAAAGTATGAAAAGTATGAAAAGT 779  
 |||||  
 DB 719 AATTAATTTTACAGATATGATGAAAAGTATGAAAAGTATGAAAAGTATGAAAAGT 778  
 |||||  
 QY 780 AAAAAAAGATTTTGTCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 839  
 |||||  
 DB 779 AAAAAAAGATTTTGTCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 838  
 |||||  
 QY 840 ACAACAGATGCTGCGCGCAACAACCAACCAACCAACCAACCAACCAACCAACCAAC 899  
 |||||  
 DB 839 ACAACAGATGCTGCGCGCAACAACCAACCAACCAACCAACCAACCAACCAACCAAC 898  
 |||||

RESULT 8  
 ID ADK5377 standard; DNA; 719 BP.

AC ADK5377;  
 DT 06-MAY-2004 (first entry)

DE Plant DNA sequence which confers altered metabolic characteristic #2760.

XX altered metabolic characteristic; plant; acid metabolism;  
 KW alcohol metabolism; fatty acid metabolism;  
 KW branched fatty acid metabolism; alkaloid metabolism;  
 KW amino acid metabolism; ester metabolism; glyceride metabolism;  
 KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;  
 KW terpene metabolism; isoprenoid metabolism; alkene metabolism;  
 KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;  
 KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.

OS Unidentified.

PN WO2003020936-A1.

PD 13-MAR-2003.

PF 30-AUG-2002; 2002WO-US027884.

PR 31-AUG-2001; 2001US-0316471P.

PA (DOWC ) DOW CHEM CO.  
 PA (DOWC ) DOW AGROSCIENCES LLC.

XX Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ,  
 PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrina I, Miller BA;  
 XX MPI; 2003-313091/30.  
 DR  
 XX Novel genes that confer altered metabolic characteristics in Nicotiana  
 PT benthamiana plants, useful for altering the levels of metabolites e.g.  
 PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.  
 XX  
 PS Claim 1; SEQ ID NO 2760; 2576bp; English.  
 XX  
 CC The invention comprises DNA sequences which confer an altered metabolic  
 CC characteristic when they are expressed in a plant. The DNA sequences of  
 CC the invention are useful for producing plants with an altered metabolic  
 CC characteristic, such as: altered acid metabolism, alcohol metabolism,  
 CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other  
 CC base metabolism, altered amino acid metabolism, altered ester metabolism,  
 CC altered glyceride metabolism, altered phenolic metabolism, altered  
 CC carbohydrate metabolism, altered sterol, oxygenated terpene, or  
 CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon  
 CC metabolism, ketone or quinone metabolism. The DNA sequences of the  
 CC invention may be used to provide disease resistance in a plant and gene  
 CC shuffling or sexual PCR procedures. The present nucleic acid represents a  
 CC DNA sequence of the invention.

SO Sequence 719 BP; 180 A; 183 C; 171 G; 185 T; 0 U; 0 Other;

Query Match 5.8%; Score 126.8; DB 10; Length 719;  
 Best Local Similarity 97.9%; Pred. No. 2.9e-18;  
 Matches 139; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1022 AGGAGCATCAAGCAAGCAAGGAGAGAGACCAAGCAAGCAAGCAAGCAAGCAAG 1081  
 |||||  
 DB 7 AGGAGCATCAAGCAAGCAAGGAGAGAGACCAAGCAAGCAAGCAAGCAAGCAAG 66  
 |||||  
 QY 1082 GCGACCGCTTCTTGATCATATCTTCGATGAGGTTCTTGATGATCTTCTCTCT 1141  
 |||||  
 DB 67 GCGACCGCTTCTTGATCATATCTTCGATGAGGTTCTTGATGATCTTCTCTCT 125  
 |||||  
 QY 1142 CCACCTCTCTCTCAACGGGTAT 1163  
 |||||  
 DB 126 CCACCTCTCTCTCAACGGGTCT 147  
 |||||

RESULT 9  
 ID ADD16740 standard; DNA; 724 BP.

AC ADD16740;  
 DT 15-JAN-2004 (first entry)

DE DNA (SegID 808) that confers an altered visual phenotype in plants.

XX ds: visual phenotype; plant; architecture; leaf surface; chlorotic;  
 KW bleaching; etching; wet leaf; stunting; elongation; texture;  
 KW agronomic traits; growth regulation; dwarf variety; insect resistance;  
 KW heat stress; transgenic.

OS Unidentified.

PN WO2003020741-A1.

PD 13-MAR-2003.

PF 30-AUG-2002; 2002WO-US027880.

PR 31-AUG-2001; 2001US-0316326P.

PA (DOWC ) DOW CHEM CO.  
 PA (DOWC ) DOW AGROSCIENCES LLC.











Db 1201 TCCCTAGTAGAAGAAACCAAGCCCTCTTAAAGTACTTATTCATTTCTTTACCAAGC 1142  
QY 199 GGGAAATGAAATCATTTATGCTTAGAATATACCTTCATGTAAGTTAAAT 258  
Db 1141 GGGAAATGAAATGCTTAGAATATACCTTCATGTAAGTTAAAT 1082  
QY 259 TATTCAGTAGGCAATATTTGTCATCAACCTCTTCTTG-----AATTAATAATCTTTC 312  
Db 1081 TCTTTCAGGTTGCTCATGATTTATATGACATCTACGCTAACCAAGAAATACATGTTTC 1022  
QY 313 TACCTGACCTCAATGGGTAAAGAGCATATTTTAAAAAATAAGAAAGAAAT 372  
Db 1021 TACCCCAATTCAGTACATCAAGATGAGGGAACCTTTTAAAAAATAAGAAATAGG 962  
QY 373 TTCTGACGATGCGGCAAGATTTTAAACATATATATATATATATATAG 422  
Db 961 AAGAAACATTTTGAATATGTCCTTGTATGAAATATGAAATTTTG 912

RESULT 15  
ABD33574  
ID ABD33574 standard; DNA; 101954 BP.  
XX ABD33574;  
AC  
XX  
XX ABD33574;  
DT 18-NOV-2004 (first entry)  
XX  
DE Human cancer-associated (CA) gene HD07-115.  
XX  
XX Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;  
KM ds; cancer; cytostatic.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004058146-A2.  
PN  
XX  
PD 15-JUL-2004.  
XX  
PF 15-DEC-2003; 2003WO-US040081.  
XX  
PR 17-DEC-2002; 2002US-00322281.  
XX  
PA (SAGR-) SAGRES DISCOVERY INC.  
XX  
PI Morris DM, Malandro MS;  
XX  
XX MPI; 2004-499109/47.  
DR  
XX  
XX Novel human cancer associated protein encoded within open reading frame  
PT of cancer associated gene, useful as targets for diagnosing cancer.  
XX  
PS Claim 16; SEQ ID NO 782, 1822pp; English.  
XX  
XX The invention relates to cancer-associated proteins (CAP) and the cancer-  
CC associated (CA) nucleic acids encoding them. The invention also relates  
CC to a method for treating cancers involving administering to a patient an  
CC inhibitor of CAP, and a method of screening for anticancer activity in a  
CC potential drug involving providing a cell that expresses a CA gene,  
CC contacting a tissue sample derived from a cancer cell with an anticancer  
CC drug candidate and monitoring the effect of the anticancer drug candidate  
CC on expression of the CA gene. The CAP proteins are useful for detecting  
CC cancer associated with expression of a CAP protein in a test cell sample  
CC and for screening for a bioactive agent capable of modulating the  
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing  
CC cancer, involving determining the expression of a CA nucleic acid in a  
CC tissue. This sequence represents a human CA gene of the invention. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 101954 BP; 29500 A; 18891 C; 19534 G; 32684 T; 0 U; 1345 Other;  
SQ

Query Match 2.5%; Score 55.6; DB 13; Length 101954;

Best Local Similarity 50.6%; Pred. No. 0.1;  
Matches 162; Conservative 0; Mismatches 154; Indels 4; Gaps 1;  
QY 225 AATATACGTTCAATCTCTGTCATGAAGTTAAATATTATGAGGTAGCCATAATGTCATC 284  
Db 74856 AACATGAGTGAACCGCTCTCTCAAAAATAATATATATATGTGTTGTATGTATATATAA 74915  
QY 285 AAACCTCTCTGTAATAAAAAAATCTTCTAGCTGAACCTCAATGGGTAAAGAGATATTT 344  
Db 74916 AATATATATATAATATAATATAATATAATATAATATAATATAATATAATATAAT 74975  
QY 345 TTTTAAAAAATAAGATGAATATCTGAAACGTATCGGCAAGATTAAACATAT 404  
Db 74976 TAAATATATATAAATAATATAATATAATATAATATAATATAATATAATATAAT 75035  
QY 405 AATATATATATTTTATAGTTTGTGATCGCTTATATTCGACGTCATTAAGACATGCTT 464  
Db 75036 AATATATATGATATATATATATATATAATATATATATATATATATATATATATAT 75095  
QY 465 ACTGCATCTCAAT---TTTATTTAGTAAATTAAGACAAATTGACTTATTTTATATTT 520  
Db 75096 TCTTTAAGGGAAGCTACTTTCTTTCCTGACAAATAGTAGTACGTTTATATAATAT 75155  
QY 521 ATCTTTTTCGATTGATGC 540  
Db 75156 GTTTTATCTTTTAGTGC 75175

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Job time : 1231 secs

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OM nucleic - nucleic search, using SW model

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Total number of hits satisfying chosen parameters: 18577160

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	1166	53.1	1176	14	US-11-128-549-2
3	1099.2	50.1	1112	14	US-11-128-549-1
4	987.8	45.0	999	14	US-11-128-549-5
5	51.8	2.5	171486	4	US-11-121-086-105
6	49.6	2.3	672	6	US-09-925-065A-673832
7	49.2	2.2	906	11	US-11-096-568A-21310
8	49.2	2.2	1739	9	US-10-893-483-184
9	49	2.2	36259	9	US-10-893-483-186
10	49	2.2	39794	14	US-11-098-686-8737
11	48.4	2.2	6152	14	US-11-196-400-1
12	48.4	2.2	624	6	US-09-925-065A-946580
13	48.2	2.2	995	10	US-10-301-480-546623
14	48.2	2.2	995	10	US-10-301-480-1160032
15	48.2	2.2	997	10	US-10-301-480-546624
16	48.2	2.2	997	10	US-10-301-480-1160033
17	48.2	2.2	997	10	US-10-301-480-1160033
18	47.6	2.2	591	6	US-09-925-065A-387578

C	19	47.6	2.2	591	6	US-09-925-065A-387580	Sequence 387580,
	20	47.6	2.2	595	10	US-10-301-480-456079	Sequence 456079,
	21	47.6	2.2	595	10	US-10-301-480-456081	Sequence 456081,
	22	47.6	2.2	595	10	US-10-301-480-1069488	Sequence 1069488,
	23	47.6	2.2	595	10	US-10-301-480-1069490	Sequence 1069490,
	24	47.6	2.2	807	10	US-10-301-480-586745	Sequence 586745,
	25	47.6	2.2	807	10	US-10-301-480-1200154	Sequence 1200154,
	26	47.4	2.2	590	9	US-10-301-480-59750	Sequence 59750, A
	27	47.4	2.2	590	9	US-10-301-480-59751	Sequence 59751, A
	28	47.4	2.2	590	9	US-10-301-480-59753	Sequence 59753, A
	29	47.4	2.2	590	10	US-10-301-480-673159	Sequence 673159,
	30	47.4	2.2	590	10	US-10-301-480-673160	Sequence 673160,
	31	47.4	2.2	590	10	US-10-301-480-673162	Sequence 673162,
	32	47.4	2.2	670	10	US-10-301-480-561044	Sequence 561044,
	33	47.4	2.2	670	10	US-10-301-480-1174453	Sequence 1174453,
	34	47.2	2.2	591	6	US-09-925-065A-387579	Sequence 387579,
	35	47.2	2.2	595	10	US-10-301-480-456080	Sequence 456080,
	36	47.2	2.2	595	10	US-10-301-480-1069489	Sequence 1069489,
	37	47	2.1	590	9	US-10-301-480-59752	Sequence 59752, A
	38	47	2.1	590	10	US-10-301-480-673161	Sequence 673161,
	39	46.8	2.1	105550	8	US-10-995-561-13335	Sequence 13335, A
	40	46.8	2.1	194553	14	US-11-098-686-8738	Sequence 8738, Ap
	41	46.6	2.1	26772	8	US-10-995-561-13313	Sequence 13313, A
	42	46.6	2.1	54946	8	US-10-995-561-13479	Sequence 13479, A
	43	46.4	2.1	585	6	US-09-925-065A-336359	Sequence 336359,
	44	46.4	2.1	585	6	US-09-925-065A-336360	Sequence 336360,
	45	46.4	2.1	602	10	US-10-301-480-409672	Sequence 409672,

## ALIGNMENTS

RESULT 1  
US-10-541-315-1  
Sequence 1, Application US/10541315  
Publication No. US2006003507A1  
GENERAL INFORMATION:  
APPLICANT: CiproDesign N.V.  
TITLE OF INVENTION: Regulatory sequence  
FILE REFERENCE: CD-072-PCT  
CURRENT APPLICATION NUMBER: US/10/541, 315  
PRIOR FILING DATE: 2005-06-30  
PRIOR APPLICATION NUMBER: EP 03075207.5  
PRIOR FILING DATE: 2003-01-21  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 2195  
TYPE: DNA  
ORGANISM: Oryza sativa  
US-10-541-315-1

Query Match 100.0%; Score 2195; DB: 9; Length 2195;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AATCGAAGTTCTGCA	CGTTTCA	CGTCTTA	CAATATAGGA	AGTGTGCT	60
DB	1	AATCGAAGTTCTGCA	CGTTTCA	CGTCTTA	CAATATAGGA	AGTGTGCT	60
QY	61	AAATATAATGAGAC	CTTATATAG	TACGCGT	ATAGTAAGAA	AACT	120
DB	61	AAATATAATGAGAC	CTTATATAG	TACGCGT	ATAGTAAGAA	AACT	120
QY	121	CATCCACCTTACTT	AGGCAATCG	GGCTTAAT	AAAAAGATCG	TACATGTTGGT	180
DB	121	CATCCACCTTACTT	AGGCAATCG	GGCTTAAT	AAAAAGATCG	TACATGTTGGT	180
QY	181	TTTCCCTTAAATTA	TAGGGAATGA	AAATCAATTA	TTCCTTAAGAT	TACGTTCAATC	240
DB	181	TTTCCCTTAAATTA	TAGGGAATGA	AAATCAATTA	TTCCTTAAGAT	TACGTTCAATC	240
QY	241	TTTCCCTTAAATTA	TAGGGAATGA	AAATCAATTA	TTCCTTAAGAT	TACGTTCAATC	300

|||||  
Db 241 TCTGTCATGAAAGTTAAATTAATCGAGGTAGCCATAATGTCATCAAACTCTCTTGAAMA 300  
Qy 301 AAAAAATCTTTAGCTGAACCTCAATGGGTAAGAGATATTTTTTTTTAAAAAAAT 360  
Db 301 AAAAAATCTTTAGCTGAACCTCAATGGGTAAGAGATATTTTTTTTTAAAAAAAT 360  
Qy 361 AGAATGAGATATTTCTGAACGTAACGCAAAAGTTTAAACATTAATTAATATTTAT 420  
Db 361 AGAATGAGATATTTCTGAACGTAACGCAAAAGTTTAAACATTAATTAATATTTAT 420  
Qy 421 AGTTTGTGATTTGTTATATCGCAGCTGATTAAGACATGCTTACTCCATCTCAATTT 480  
Db 421 AGTTTGTGATTTGTTATATCGCAGCTGATTAAGACATGCTTACTCCATCTCAATTT 480  
Qy 481 TATTTAGTATTAAGCAATGACTTAATTTTATTAATTAATCTTTTTCGATTAGATC 540  
Db 481 TATTTAGTATTAAGCAATGACTTAATTTTATTAATTAATCTTTTTCGATTAGATC 540  
Qy 541 AAGGTACTTAACGACACACTTTGTGCTCATGTGATGATGTGACCTCTCATACAC 600  
Db 541 AAGGTACTTAACGACACACTTTGTGCTCATGTGATGATGTGACCTCTCATACAC 600  
Qy 601 GTTCAACTAGCGACACATCTCCATATCACTGGCTATTTAATACATTAAGTACAA 660  
Db 601 GTTCAACTAGCGACACATCTCCATATCACTGGCTATTTAATACATTAAGTACAA 660  
Qy 661 TCTGAATTAAGACACTTACCATCACAGACCACTTTTAATATCTAAATACAAAA 720  
Db 661 TCTGAATTAAGACACTTACCATCACAGACCACTTTTAATATCTAAATACAAAA 720  
Qy 721 ATTAATTTTACAGATAGCATGAAAGATGAAAGCAATATTTAGTTTTCATACAA 780  
Db 721 ATTAATTTTACAGATAGCATGAAAGATGAAAGCAATATTTAGTTTTCATACAA 780  
Qy 781 AAAAAAAGAAATTTTGTCTGTGCGGAGGCGCAATCTCCCATTTGGGACACAGGAA 840  
Db 781 AAAAAAAGAAATTTTGTCTGTGCGGAGGCGCAATCTCCCATTTGGGACACAGGAA 840  
Qy 841 CAACAGATGGGCTGCCACAGAACCCCAAAAAAGATGATCTAACAGAGACAGCA 900  
Db 841 CAACAGATGGGCTGCCACAGAACCCCAAAAAAGATGATCTAACAGAGACAGCA 900  
Qy 901 AGTCCGCAACACCTTTTAAACAGACAGCTTTGGGCGCAGAGAGAGAGAGGCAAG 960  
Db 901 AGTCCGCAACACCTTTTAAACAGACAGCTTTGGGCGCAGAGAGAGAGAGGCAAG 960  
Qy 961 AAAACCAAGATCTCTCTCTCCCATCTAATAATTTCTCCCTTTTCCCTCTCTATA 1020  
Db 961 AAAACCAAGATCTCTCTCTCCCATCTAATAATTTCTCCCTTTTCCCTCTCTATA 1020  
Qy 1021 TAGGAGGACATCCAAAGCAAGAAAGGAGAGACCAAGGACACGCACTAGCAGAACCG 1080  
Db 1021 TAGGAGGACATCCAAAGCAAGAAAGGAGAGACCAAGGACACGCACTAGCAGAACCG 1080  
Qy 1081 AAGGACCGGCTTCTTGATCATATCTTCGAGTCTTGAGTCTTCTCCCTCC 1140  
Db 1081 AAGGACCGGCTTCTTGATCATATCTTCGAGTCTTGAGTCTTCTCCCTCC 1140  
Qy 1141 TCCACTCTCTCTCAACAGGATATGCGCTTGGTTTCTTGAGATTTATGTTCTAAGT 1200  
Db 1141 TCCACTCTCTCTCAACAGGATATGCGCTTGGTTTCTTGAGATTTATGTTCTAAGT 1200  
Qy 1201 TGTGTATGTAACGGGCTTGATGTTAGAAAGGGGATCTGATCTGTATGATTTCTGTCT 1260  
Db 1201 TGTGTATGTAACGGGCTTGATGTTAGAAAGGGGATCTGATCTGTATGATTTCTGTCT 1260  
Qy 1261 TGGATTTGGGATAGAGGGGTTCTTGATGTTGATGTTATCGGTTGGTTAGTATGAT 1320  
Db 1261 TGGATTTGGGATAGAGGGGTTCTTGATGTTGATGTTATCGGTTGGTTAGTATGAT 1320  
Qy 1321 ATGTTTTCATGCTCTGAGAGCTCTATGAGAAATGAATGTTTAGGGTACGGAATCTT 1380  
|||||

Db 1321 ATGTTTTCATGCTCTGAGAGCTCTATGAGAAATGAATGTTTAGGGTACGGAATCTT 1380  
Qy 1381 GCGATTTGTGATGATACCTTTTGTGAGTAATAACAGACACCGGTGATTTGTGCTGT 1440  
Db 1381 GCGATTTGTGATGATACCTTTTGTGAGTAATAACAGACACCGGTGATTTGTGCTGT 1440  
Qy 1441 GTTAATTAAGTACATTTGTGTTGCTGATCTCTGTAGTATGCTTCTCGATTTGACGA 1500  
Db 1441 GTTAATTAAGTACATTTGTGTTGCTGATCTCTGTAGTATGCTTCTCGATTTGACGA 1500  
Qy 1501 AGCTATCCTTTGTTATTTCCCTAATGAACAAATAATCAACTTTGGAAGACGCTCCGT 1560  
Db 1501 AGCTATCCTTTGTTATTTCCCTAATGAACAAATAATCAACTTTGGAAGACGCTCCGT 1560  
Qy 1561 TGATGAGATGTAATGATGATTTCTTAAGCTGTCCAAAATTTGCGAGCTGGCTTTAG 1620  
Db 1561 TGATGAGATGTAATGATGATTTCTTAAGCTGTCCAAAATTTGCGAGCTGGCTTTAG 1620  
Qy 1621 ATACAGTATGCTCCCATCAAGAAATTCATGAAACAGTTATATCTTCAGGAAACAGGGAT 1680  
Db 1621 ATACAGTATGCTCCCATCAAGAAATTCATGAAACAGTTATATCTTCAGGAAACAGGGAT 1680  
Qy 1681 TCCCTGTTCTCCGATTTGCTTATGTCAGAAATTTTTCGAAATATCTTAAAGT 1740  
Db 1681 TCCCTGTTCTCCGATTTGCTTATGTCAGAAATTTTTCGAAATATCTTAAAGT 1740  
Qy 1741 CACTTGTGTTCACTTCAATGAATGATTTGCTACAAATATATGCTTTTATAGCGTTATCC 1800  
Db 1741 CACTTGTGTTCACTTCAATGAATGATTTGCTACAAATATATGCTTTTATAGCGTTATCC 1800  
Qy 1801 TGTGCTGATGATGATTTATAGTATATCCCTATAGTTTATGTCAGAGAAAGAACTTATCC 1860  
Db 1801 TGTGCTGATGATGATTTATAGTATATCCCTATAGTTTATGTCAGAGAAAGAACTTATCC 1860  
Qy 1861 GATTTCTGATCTCCATTTTATTAATTAATGAATGAAGTATGATGATGATGATGAT 1920  
Db 1861 GATTTCTGATCTCCATTTTATTAATTAATGAATGAAGTATGATGATGATGATGAT 1920  
Qy 1921 GGATTAATTTTATTAATGATTTTCAACCCCTTCAATTTCTGAGCTGAAGAGTCTGACATGA 1980  
Db 1921 GGATTAATTTTATTAATGATTTTCAACCCCTTCAATTTCTGAGCTGAAGAGTCTGACATGA 1980  
Qy 1981 ACTGTCCTCAATTTGTTTCAAAATTCACATGATGATGATGATGATGATGATGATGAT 2040  
Db 1981 ACTGTCCTCAATTTGTTTCAAAATTCACATGATGATGATGATGATGATGATGATGAT 2040  
Qy 2041 TACCTGTGAAGTCTTTTGTGTTATCTTGAATGATGATGATGATGATGATGATGATGAT 2100  
Db 2041 TACCTGTGAAGTCTTTTGTGTTATCTTGAATGATGATGATGATGATGATGATGATGAT 2100  
Qy 2101 GAAGCTGATATCGGATAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2160  
Db 2101 GAAGCTGATATCGGATAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2160  
Qy 2161 CTGCTGTGATGCTTGCACCTTTTACACGAAAGTTC 2195  
Db 2161 CTGCTGTGATGCTTGCACCTTTTACACGAAAGTTC 2195  
  
RESULT 2  
US-11-128-549-2  
; Sequence 2, Application US/11128549  
; Publication No. US20050262597A1  
; GENERAL INFORMATION:  
; APPLICANT: Broekaert, Willem  
; APPLICANT: De Wilde, Chris  
; APPLICANT: Hatzfeld, Yves  
; APPLICANT: Zhou, Zhongyi  
; TITLE OF INVENTION: METHOD FOR INCREASING TRANSGENE EXPRESSION  
; FILE REFERENCE: 1187-40  
; CURRENT APPLICATION NUMBER: US/11/128,549  
; PRIORITY FILING DATE: 2005-05-13  
; PRIOR APPLICATION NUMBER: US 60/572,141



DB 301 GGTACGGATCTTGCATTTTGGAGTACCTTTGTTAGGTAATAATAGACACCGGT 360  
1428 GATTTTGTGGTGTATATAAGTACATTTGTTGGTCTCGATTCGGTAGTATGCTT 1487  
DB 361 GATTTTGTGGTGTATATAAGTACGATTTGTTGGTCTCGATTCGGTAGTATGCTT 420  
1488 CTGATTTTGAAGGATCTATCTTTGTTTATTCCTATTTGAACAATAATATCCACTTTG 1547  
DB 421 CTGATTTTGAAGGATCTATCTTTGTTTATTCCTATTTGAACAATAATATCCACTTTG 480  
1548 AAGACGGTCCGTTGATGATTTGAATGATTTGATTTCTTAAAGCTGTCCAAATTTGGCG 1607  
DB 481 AAGACGGTCCGTTGATGATTTGAATGATTTGATTTCTTAAAGCTGTCCAAATTTGGCG 540  
1608 CTGGCTTTGTTAGATCAGATGATCCCATCAAGAAATTCATGAAAACAGTTTAAATCTTC 1667  
DB 541 CTGGCTTTGTTAGATCAGATGATCCCATCAAGAAATTCATGAAAACAGTTTAAATCTTC 600  
1668 AAGAAACAGGGGATTCCTGTTCTTCGATTTTGTAGTCCAGAAATTTTTCGCAAA 1727  
DB 601 AAGAAACAGGGGATTCCTGTTCTTCGATTTTGTAGTCCAGAAATTTTTCGCAAA 660  
1728 TATCTTAAAAAGTCACTTTCTGTTGATTTCAATGAAATTTGATTTGCTACAAATATGCTTT 1787  
DB 661 TATCTTAAAAAGTCACTTTCTGTTGATTTCAATGAAATTTGATTTGCTACAAATATGCTTT 720  
1788 TATAGGTTATCTTACGATGATTTCAATGATTTCAATGATTTCAATGATTTCAATGATTT 1847  
DB 721 TATAGGTTATCTTACGATGATTTCAATGATTTCAATGATTTCAATGATTTCAATGATTT 780  
1848 GAAGAATTATCCGATTTCTGATTTCTCAATTTTAAATATGAAATGAACTGTAGCATTA 1907  
DB 781 GAAGAATTATCCGATTTCTGATTTCTCAATTTTAAATATGAAATGAACTGTAGCATTA 840  
1908 GAGATATTTGATTTGATTTATTTTATTTAGTTTCACTTCACTTCACTTCACTTCACTT 1967  
DB 841 GAGATATTTGATTTGATTTATTTTATTTAGTTTCACTTCACTTCACTTCACTTCACTT 900  
1968 AAGTCCGATGAACTGCTCTCAATTTTGTTCGAATTCAGATGATTTCACTTCACTT 2027  
DB 901 AAGTCCGATGAACTGCTCTCAATTTTGTTCGAATTCAGATGATTTCACTTCACTT 960  
2028 ATCTCTTGTATCTACCTGTAGAAAGTTTCTTTTGTATATCTTGTAGCTGTATTA 2087  
DB 961 ATCTCTTGTATCTACCTGTAGAAAGTTTCTTTTGTATATCTTGTAGCTGTATTA 1020  
2088 GAAAGAAATTTATGAAGCTGTATATCGGATAGTTATATCTGTTGTTCTTATGATTCATT 2147  
DB 1021 GAAAGAAATTTATGAAGCTGTATATCGGATAGTTATATCTGTTGTTCTTATGATTCATT 1080  
2148 CCTTTGTGAGTTCTTGTGTAGCTTGCACCT 2179  
DB 1081 CCTTTGTGAGTTCTTGTGTAGCTTGCACCT 1112

RESULT 4  
US-11-128-549-5  
; Sequence 5, Application US/11128549  
; Publication No. US20050262597A1  
; GENERAL INFORMATION:  
; APPLICANT: Broekert, Willem  
; APPLICANT: De Wilde, Chris  
; APPLICANT: Hatzfeld, Yves  
; APPLICANT: Zhou, Zhongyi  
; TITLE OF INVENTION: METHOD FOR INCREASING TRANSGENE EXPRESSION  
; FILE REFERENCE: 1187-40  
; CURRENT APPLICATION NUMBER: US/11128,549  
; CURRENT FILING DATE: 2005-05-13  
; PRIOR APPLICATION NUMBER: US 60/572,141  
; PRIOR FILING DATE: 2004-05-18  
; PRIOR APPLICATION NUMBER: EP 04102108.0  
; PRIOR FILING DATE: 2004-05-13

; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 5  
; LENGTH: 999  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
US-11-128-549-5  
Query Match 45.0%; Score 987.8; DB 14; Length 999;  
Best Local Similarity 99.3%; Pred. No. 5,1e-184;  
Matches 992; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
DB 1180 GATATGCTTCCTGCTGTTGTTCTTGGATTTATTTGTTCTAGAGTTTGTATAGCGGGCTTGA 1219  
1 GATATGCTTCCTGCTGTTGTTCTTGGATTTATTTGTTCTAGAGTTTGTATAGCGGGCTTGA 60  
DB 1220 TGTAGAAAGGGGATCTGTATCTGTATGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1279  
61 TGTAGAAAGGGGATCTGTATCTGTATGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 120  
DB 1280 TTTCTGATGTTGATGATTTATCGGTTCTGTTGATTTAGTATGATTTGATTTGATTTGATTTG 1339  
121 TTTCTGATGTTGATGATTTATCGGTTCTGTTGATTTAGTATGATTTGATTTGATTTGATTTG 180  
DB 1340 AAGCTCTATGAAATGAAATGATTTAGGTTAGCGGAATCTTGCATTTTGTAGTATCTT 1339  
181 AAGCTCTATGAAATGAAATGATTTAGGTTAGCGGAATCTTGCATTTTGTAGTATCTT 240  
DB 1400 TTTGTTAGGTTAAATCAGACACCGGATTTTGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1459  
241 TTTGTTAGGTTAAATCAGACACCGGATTTTGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 300  
DB 1460 TTTGCTCTGATTTCTGATGATTTCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1519  
301 TTTGCTCTGATTTCTGATGATTTCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 360  
DB 1520 CCTATTTGAAACAAATATATCCAACTTTGAAACAGGTCCTGTTGATTTGATTTGATTTGATTTG 1579  
361 CCTATTTGAAACAAATATATCCAACTTTGAAACAGGTCCTGTTGATTTGATTTGATTTGATTTG 420  
DB 1580 ATTCTTAAAGCTGTCCAAATTTTGTGAGCTGTTGTTGATTTGATTTGATTTGATTTGATTTG 1639  
421 ATTCTTAAAGCTGTCCAAATTTTGTGAGCTGTTGTTGATTTGATTTGATTTGATTTGATTTG 480  
DB 1640 GAAATTTCAATGAAACAGTTATATCTCAGAAACAGGGGATTTCCCTGTTCTTCGATTTG 1699  
481 GAAATTTCAATGAAACAGTTATATCTCAGAAACAGGGGATTTCCCTGTTCTTCGATTTG 540  
DB 1700 CTTTATGCTCCGAAATTTTTCCTCAATATCTTAAATATGATTTGATTTGATTTGATTTGATTTG 1759  
541 CTTTATGCTCCGAAATTTTTCCTCAATATCTTAAATATGATTTGATTTGATTTGATTTGATTTG 600  
DB 1760 ATGAATGATTTGCTACAAATATGCTTTATAGGTTATCTTACGATTTGATTTGATTTGATTTG 1819  
601 ATGAATGATTTGCTACAAATATGCTTTATAGGTTATCTTACGATTTGATTTGATTTGATTTG 660  
DB 1820 AAGTATATCCCTATATGTTATGTCAGAGAAAGAACTTATCCGATTTGATTTGATTTGATTTG 1879  
661 AAGTATATCCCTATATGTTATGTCAGAGAAAGAACTTATCCGATTTGATTTGATTTGATTTG 720  
DB 1880 TATATTTATGAAATGAACTGTAGCATTAAGCATTTATCTTGTGATTTATTTTATTTATTTAG 1939  
721 TATATTTATGAAATGAACTGTAGCATTAAGCATTTATCTTGTGATTTATTTTATTTATTTAG 780  
DB 1940 CTTTCAAGCTCTTATTTATGATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1999  
781 CTTTCAAGCTCTTATTTATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 840  
DB 2000 TCAATTTCAATGATTTATCTATGATTTATCTTGTGATTTATCTTGTGATTTATTTGATTTG 2059  
841 TCAATTTCAATGATTTATCTATGATTTATCTTGTGATTTATCTTGTGATTTATTTGATTTG 900  
DB 2060 TTTGTTATTTCTTGTATCTGATTTATGAAAGAAATTTATGAAAGCTGTATCTGAGATAG 2119





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/ APPLICANT: Wang, David G.  
/ TITLE OF INVENTION: Identification and Mapping of Single  
/ FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome  
/ CURRENT APPLICATION NUMBER: US 60/925,065A  
/ CURRENT FILING DATE: 2001-08-08  
/ PRIOR APPLICATION NUMBER: US 60/243,096  
/ PRIOR FILING DATE: 2000-10-24  
/ PRIOR APPLICATION NUMBER: US 60/252,147  
/ PRIOR FILING DATE: 2000-11-20  
/ PRIOR APPLICATION NUMBER: US 60/250,092  
/ PRIOR FILING DATE: 2000-11-30  
/ PRIOR APPLICATION NUMBER: US 60/261,766  
/ PRIOR FILING DATE: 2001-01-16  
/ PRIOR APPLICATION NUMBER: US 60/289,846  
/ PRIOR FILING DATE: 2001-05-09  
/ NUMBER OF SEQ ID NOS: 957086  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 673832  
/ LENGTH: 672  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
US-09-925-065A-673832
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Query Match 2.3%; Score 49.6; DB 6; Length 672;  
Best Local Similarity 47.2%; Pred. No. 4.5;  
Matches 185; Conservative 1; Mismatches 200; Indels 6; Gaps 1;
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QY 155 AAAAAGAGCGCTACCTAGTTCCGTTCCCTAGTAATTAAGTGAAGAATCAT 214  
DB 418 ATTAATAAATAATACCTTTTGTATATAAATAAATAATATTTATATAATAATA 359  
QY 215 TATTCCTAGAAATATACCTTCATCATCTGTCATGAAATTAATTCAGAGTACCAT 274  
DB 358 TATTCCTAATATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 299  
QY 275 AATGTCATCAAACTCTCTCTGTAATAAATAATCTTTGACCTGAACCTCAATGGGTAAG 334  
DB 298 AATATATATAA-----TATTAATGAATAATACATATCTTTATATATAATATATATAT 245  
QY 335 AAGAGATATTTTTTTTAAATAAATAAATGAAGATATTCGAACGTATCGGCAAGAT 394  
DB 244 ACATATAATATATATTTTCCATATAAATAAATAATACATATTTTATATATTA 185  
QY 395 TTAACATATATATATATATATATATATATATATATATATATATATATATATAT 454  
DB 184 TATATATATATAAATAATTTTATATATATATATATATATATATATATATATAT 125  
QY 455 GACATGCTTACTCCATCTCAATTTTATATTAAGTAATAAGCAATGACTTATTTTA 514  
DB 124 TATTTATATATAATATATATATATATATATATATATATATATATATATATAT 65  
QY 515 TTAATTAATCTTTTTCGATTAGATGAAGTA 546  
DB 64 TATATATATATATTTTATATATATATATATTTTA 33
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RESULT 8  
US-11-096-568A-21310  
/ Sequence 21310, Application US/11096568A  
/ Publication No. US20060048240A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Alexandrov, Nikolai et al.  
/ TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
/ FILE REFERENCE: 2750-1592PUS2  
/ CURRENT APPLICATION NUMBER: US/11/096,568A  
/ CURRENT FILING DATE: 2005-04-01  
/ NUMBER OF SEQ ID NOS: 34471  
/ SEQ ID NO 21310  
/ LENGTH: 906  
/ TYPE: DNA  
/ ORGANISM: Zea mays subsp. mays
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/ FEATURE:  
/ NAME/KEY: misc_feature  
/ LOCATION: (1)..(906)  
/ OTHER INFORMATION: Ceres Seq. ID no. 12402928  
US-11-096-568A-21310
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Query Match 2.2%; Score 49.2; DB 11; Length 906;  
Best Local Similarity 80.4%; Pred. No. 5.9;  
Matches 82; Conservative 0; Mismatches 18; Indels 2; Gaps 2;
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QY 968 AGCATCTCTCCCTCCCATATATAATTCCTCCCTCTCTATATAGAG 1027  
DB 80 ACCGCTCTCTCTCTCCCTCTATTAATTC--CTCTTTTCTCTCTCATATATAGGGC 138  
QY 1028 CATCCAGCCAAAGAGAGG--AGAGCACCAAGACACCGGAC 1068  
DB 139 CATCAGATCCAAAGAGAGGAGAGACCAAGACCTTCGGC 180
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RESULT 9  
US-10-893-483-184  
/ Sequence 184, Application US/10893483  
/ Publication No. US20060026696A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Buelow, Roland  
/ APPLICANT: Plazzer, Josef  
/ APPLICANT: Schooten, Wim van  
/ TITLE OF INVENTION: Humanized Immunoglobulin Loc1  
/ FILE REFERENCE: 39691-0007A  
/ CURRENT APPLICATION NUMBER: US/10/893,483  
/ CURRENT FILING DATE: 2004-07-15  
/ PRIOR APPLICATION NUMBER: 60/487,733  
/ PRIOR FILING DATE: 2003-07-15  
/ NUMBER OF SEQ ID NOS: 460  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 184  
/ LENGTH: 1739  
/ TYPE: DNA  
/ ORGANISM: Gallus domesticus  
US-10-893-483-184
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Query Match 2.2%; Score 49; DB 9; Length 1739;  
Best Local Similarity 52.2%; Pred. No. 8.1;  
Matches 109; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
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QY 326 TGGGTAAGAGAGATTTTTTTTAAATAAATAAATGAATGAGATATTCGAACGTATC 385  
DB 507 TGTCAAAAAGAGAGGTATTCCTGTAAGAGAGGAAATTTTGTCAATTTTTT 566  
QY 386 GGCAGAGATTTAAACATATAATTAATTAATTAATTAATTAATTAATTAATTAAT 445  
DB 567 CGGAATATATATATATATATATATATATATATATATATATATATATATATAT 626  
QY 446 GTCAATTAAGAGATCTTACTCCATCTCAATTTTATATTAAGTAATAAGCAATGAC 505  
DB 627 TATATATATAAATAATATATATATATATATATATATATATATATATATATAT 686  
QY 506 TTAATTAATTAATTAATCTTTTTCGATT 534  
DB 687 ATATTTCTCCCTCTTTCTTTATATATATT 715
```

```
RESULT 10  
US-10-893-483-186  
/ Sequence 186, Application US/10893483  
/ Publication No. US20060026696A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Buelow, Roland  
/ APPLICANT: Plazzer, Josef  
/ APPLICANT: Schooten, Wim van  
/ TITLE OF INVENTION: Humanized Immunoglobulin Loc1  
/ FILE REFERENCE: 39691-0007A  
/ CURRENT APPLICATION NUMBER: US/10/893,483
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:
: CURRENT FILING DATE: 2004-07-15
: PRIOR APPLICATION NUMBER: 60/487, 733
: PRIOR FILING DATE: 2003-07-15
: NUMBER OF SEQ ID NOS: 460
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 186
: LENGTH: 36259
: TYPE: DNA
: ORGANISM: Gallus domesticus
: US-10-893-483-186

```

Query Match	2.2%	Score 49;	DB 9;	Length 36259;
Best Local Similarity	52.2%;	Pred. No. 23;		
Matches 109; Conservative	0;	Mismatches 100;	Indels 0;	Gaps 0;

<i>OY</i>	326	TGGGTAAAGGAGATATTTTTTTTAAAAAAAATGAATGAAGATATTCTGAACGTATC	385
<i>Db</i>	24856	TGTCAAAAAAATGGAGGTTATTCTCGTGAAAAAGCTGAGCAATATTTGTCATTTTTTT	24915
<i>OY</i>	386	GGCACAAGATTAAACATATATATTAATAATTTATATAGTTGTGCATTCGTATATTCGCAC	445
<i>Db</i>	24916	CGGAAATA	24975
<i>OY</i>	446	GTCATTAGAAGCATGTCCTTAAGTCCATCTCAATTTTATTTAGTAATTAAGACAAATTGAC	505
<i>Db</i>	24976	TATATATATAAAAATATATGATTTCTCTCTCTTTTATATATATATATATATATATATAT	25035
<i>OY</i>	506	TTATTTTATATATTAATCTTTTTCAGTT	534
<i>Db</i>	25036	ATAATTTCTCCCTTTCTTATATATATAT	25064

```

RESULT 11
US-11-098-686-8737/c
; Sequence 8737, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8737
; LENGTH: 39794
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
; US-11-098-686-8737

```

Query Match	Best Local Similarity	4.2%;	Score 49;	DB 14;	Length 39794;
Matches 145;	Conservative	0;	Mismatches 160;	Indels 0;	Gaps 0;
Qy .	191	AATTAAGTGGGAAATTAATTAATTCATTATTCGTTCGATATACGTCACATCTCTGTCATGA	250		
Db	27606	AATTAATATGTAATAAAGTTATCTTATATGCAAAAAACAAATATCAATTAAGATATCTAAT	27547		
Qy	251	AGTTAAATTTATCGAGGTACCAATATGTGCATCAAACTCTTCGTGAATATAAAAATCTT	310		
Db	27546	TAAATATATTTATTTTTCATTCACATTAATAATTAATGATATATTTATTAATTTGATTATTC	27487		
Qy	311	TCTAGCGAATCTCAATCGGTAAAGAGATATTTTTTTTAAAAAAAATAGCATGAAGA	370		
Db	27486	CATACATATGATGAATGAAGGTATTAATATATTTAAAGTGTATATTCACGTAGTTATCAAC	27422		
Qy	371	TATTCGACGTATCGGCAAAAGATTAAACATATTAATATATATTTATAGTTTGTGCA	430		

Db	27426	CTAAATATATATTTTACCTTTTGGTTCTAAATATATATTTCTAATTAATTAATTAATTTAGTTAA	27367
Oy	431	TTGCTATATACGACGCTCATTTAAGACATGTCTTACTCATCTCAATTTTTTATTTAGTAA	490
Db	27366	TTTAAATGTCATCTATTTGTAATATTTTAAATTTAATTAATTAATTAATTAATTAATTAATTTAGT	27307
Oy	491	TTAAA	495
Db	27306	TATATA	27302

RESULT 12  
US-11-196-400-1/c  
; Sequence 1, Application US/11196400  
; Publication No. US20050287166A1  
\*\*\*\*\* END \*\*\*\*\*

```

? APPLICANT: DUBIHE, PIERRE
? APPLICANT: DUBIERSIES, PIERRE
? TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
? FILE REFERENCE: 2007730501V
? CURRENT APPLICATION NUMBER: US/11/196,400
? CURRENT FILING DATE: 2005-08-04
? PRIOR APPLICATION NUMBER: US/09/742,096
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: US 08/973,462
? PRIOR FILING DATE: 1998-02-06
? PRIOR APPLICATION NUMBER: PCT/FR96/00694
? PRIOR FILING DATE: 1996-06-12
? PRIOR APPLICATION NUMBER: FR 95/07007
? PRIOR FILING DATE: 1995-06-13
? NUMBER OF SEQ ID NOS: 29
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO. 1
? LENGTH: 6152
? TYPE: DNA
? ORGANISM: P. falciparum
? OS-11-196-400-1

```

Query Match	2.2%	Score 48.4	DB 14	Length 6152
Best Local Similarity	52.5%	Pred. No. 16		
Matches 106	Conservative	0	Mismatches 96	Indels 0
			Gaps	0
QY	346	TTTTTAAAAAATATAGATGAAATGATATTCGAAAGTATCGGCAAGATTTTAAACATATA	405	
Db	5837	TTTATATATTTAAAAATATGAAATATTTAAATATATATGAAAAATATTAATATTAA	5778	
QY	406	ATTATATATTTTATAGTTTGTCATTCGTTATATCGACGTCATTAAGACATGCTTA	465	
Db	5777	TATATATTAATTTTAAATTTTAAATTTTGTAAGAAATACATATATATATATATAT	5718	
QY	466	CTCCATCTCAATTTTATTTATAGTAATTAAGACATTTACTTATTTTATTTATCTT	525	
Db	5717	ATGTATGTATTTTATTTTATTTATATATATTTACATAATATATACATTTTATATTTT	5658	
QY	526	TTTTCGATTGATGCAAGGTAC	547	
Db	5657	TTATCGATTAATTTTATGTTC	5636	

RESULT 13

US-09-925-065A-946580/C

Sequence 946580, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Mang, David G.

TITLE OR INVENTION: Identification and Mapping of Single

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925, 065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243, 096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

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/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 946580
/ LENGTH: 624
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-946580
```

```
Query Match
Best Local Similarity 55.7%; Score 48.2; DB 10; Length 624;
Matches 113; Conservative 0; Mismatches 88; Indels 2; Gaps 1;
```

```
Qy 365 TGAAGATATTCGAAAGTATCGCAAGATTTAAACATATATATATATATATAGTT 424
Db 201 TGACTTATTAATAACCTTAGCTTAACACAAACATATATAGCTATACAAAACC 142
Qy 425 TGTGATTCGTTATATCGACGTCATTAAGACATGCTTACTCCATCTCAATTTTATT 484
Db 141 TTTCTCTTTTATATATCCCTATTCCTAAAGCTCTTTCTATTTAAATTAATATTT--TT 84
Qy 485 TAGTATTTAAAGCAATTTGACTATTTTATTTATTTATCTTTTTCGATTAGTCAGG 544
Db 83 AATTATATATTTTAAATACATCTTTTATTTTAACTTTTGAATTAACATTAAGA 24
Qy 545 TACTTAGCACACACTTTGTGCT 567
Db 23 TACACACACACACACTTCACT 1
```

```
RESULT 14
US-10-301-480-546623/c
/ Sequence 546623, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ PRIOR FILING DATE: 2001-08-10
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 546623
/ LENGTH: 995
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-546623
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```
Query Match
Best Local Similarity 55.7%; Score 48.2; DB 10; Length 995;
Matches 113; Conservative 0; Mismatches 88; Indels 2; Gaps 1;
```

```
Qy 365 TGAAGATATTCGAAAGTATCGCAAGATTTAAACATATATATATATATATAGTT 424
Db 854 TGACTTATTAATAACCTTAGCTTAACACAAACATATATAGCTATACAAAACC 795
Qy 425 TGTGATTCGTTATATCGACGTCATTAAGACATGCTTACTCCATCTCAATTTTATT 484
Db 794 TTTCTCTTTTATATATCCCTATTCCTAAAGCTCTTTCTATTTAAATTAATATTT--TT 737
Qy 485 TAGTATTTAAAGCAATTTGACTATTTTATTTATTTATCTTTTTCGATTAGTCAGG 544
```

```
Db 736 AATTAAATATTTTAAATATCATCTTTTCTTTTAACTTTTGTGATTAATACTAAGA 677
Qy 545 TACTTAGCACACACTTTGTGCT 567
Db 676 TACACACACACACACTTCACT 654
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```
RESULT 15
US-10-301-480-1160032/c
/ Sequence 1160032, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ PRIOR FILING DATE: 2001-08-10
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1160032
/ LENGTH: 995
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-1160032
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```
Query Match
Best Local Similarity 55.7%; Score 48.2; DB 10; Length 995;
Matches 113; Conservative 0; Mismatches 88; Indels 2; Gaps 1;
```

```
Qy 365 TGAAGATATTCGAAAGTATCGCAAGATTTAAACATATATATATATATATAGTT 424
Db 854 TGACTTATTAATAACCTTAGCTTAACACAAACATATATAGCTATACAAAACC 795
Qy 425 TGTGATTCGTTATATCGACGTCATTAAGACATGCTTACTCCATCTCAATTTTATT 484
Db 794 TTTCTCTTTTATATATCCCTATTCCTAAAGCTCTTTCTATTTAAATTAATATTT--TT 737
Qy 485 TAGTATTTAAAGCAATTTGACTATTTTATTTATTTATCTTTTTCGATTAGTCAGG 544
Db 736 AATTAAATATTTTAAATACATCTTTTATTTTAACTTTTGAATTAATACTAAGA 677
Qy 545 TACTTAGCACACACTTTGTGCT 567
Db 676 TACACACACACACACTTCACT 654
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Search completed: April 21, 2006, 09:30:30
Job time : 2184 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 21, 2006, 09:00:48 ; Search time 1135 Seconds  
(without alignments)  
11205.332 Million cell updates/sec

Title: US-10-541-315-1

Perfect score: 2195  
Sequence: 1 aatccgaaagttctgcac.....catttcacgcaagttc 2195

Scoring tables: OLIGO\_NUS  
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size: 8

Total number of hits satisfying chosen parameters: 11765110

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : GenEmbl:\*

1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pal:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_brs:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_hcg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2195	100.0	2195	CQ876145	CQ876145 Sequence
2	1267	57.7	9361	BD251965	BD251965 Artificial
3	1267	57.7	10629	BD251966	BD251966 Artificial
4	1267	57.7	14203	AF294979	AF294979 Binary ve
5	1267	57.7	14230	AF294980	AF294980 Binary ve
6	1266	57.7	3192	OSGOS2G	XS1910 O. sativa (r
7	1168	53.2	105692	AP003953	AP003953 Oryza sat
8	1168	53.2	110000	AP008213_206	Continuation (207
9	1168	53.2	144741	AF004674	AF004674 Oryza sat
10	1165	53.1	3032	CQ895917	CQ895917 Sequence
11	936	42.6	2191	CS055056	CS055056 Sequence
12	402	18.3	898	AR643981	AR643981 Sequence
13	402	18.3	898	AX044095	AX044095 Sequence
14	402	18.3	898	AX044183	AX044183 Sequence
15	69	3.1	752	AK120697	AK120697 Oryza sat
16	65	3.0	744	AF094774	AF094774 Oryza sat
17	65	3.0	1275	AK105037	AK105037 Oryza sat
18	37	1.7	773	AF380357	AF380357 Porteresi

19	29	1.3	48	6	AR643948	AR643948 Sequence
20	29	1.3	48	6	AX044062	AX044062 Sequence
21	29	1.3	48	6	AX044162	AX044162 Sequence
22	27	1.2	12733	6	AX344992	AX344992 Sequence
23	25	1.1	216631	8	AC005332	AC005332 Homo sapi
24	25	1.1	254308	14	AC103498	AC103498 Rattus no
25	24	1.1	24	6	AX576643	AX576643 Sequence
26	24	1.1	24	6	AX576644	AX576644 Sequence
27	24	1.1	2872	2	DDIURBPB	M19492 Slime mold
28	24	1.1	37057	15	AC149333	AC149333 Phakopos
29	24	1.1	110000	15	AP008207_210	Continuation (211
30	24	1.1	153751	2	AC16551	AC16551 Dicyosbe
31	24	1.1	157943	15	AP003443	AP003443 Oryza sat
32	24	1.1	158830	15	AP003372	AP003372 Oryza sat
33	24	1.1	121574	14	AC098111	AC098111 Rattus no
34	24	1.1	122552	14	AC123312	AC123312 Rattus no
35	24	1.1	1226979	14	AC128140	AC128140 Rattus no
36	24	1.1	1227958	14	AC105532	AC105532 Rattus no
37	24	1.1	1231583	5	CR383672	CR383672 Zebrafish
38	24	1.1	124424	14	AC131614	AC131614 Rattus no
39	24	1.1	1252743	14	AC098928	AC098928 Rattus no
40	24	1.1	1254519	14	AC106458	AC106458 Rattus no
41	24	1.1	1260838	14	AC130235	AC130235 Rattus no
42	24	1.1	1292390	14	AC105677	AC105677 Rattus no
43	23	1.0	4592	15	AK100568	AK100568 Oryza sat
44	23	1.0	8842	6	AX277908	AX277908 Sequence
45	23	1.0	8842	6	AX323589	AX323589 Sequence

## ALIGNMENTS

RESULT 1	CQ876145	2195 bp	DNA	linear	PAT 04-OCT-2004
LOCUS	CQ876145	Sequence 1 from Patent WO2004065596.			
DEFINITION	CQ876145				
ACCESSION	CQ876145.1	GI:53789748			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Oryza sativa				
	Burkholderia; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.				
REFERENCE	1	Hatzfeld, Y. and Inze, D.			
AUTHORS					
TITLE	Regulatory sequence				
JOURNAL	Patent: WO 2004065596-A 1 05-AUG-2004;				
	CropDesign N.V. (BE)				
FEATURES	Location/Qualifiers				
source	1..2195				
	/organism="Oryza sativa"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:4530"				
ORIGIN					
Query Match	100.0%; Score 2195; DB 6; Length 2195;				
Best Local Similarity	100.0%; Pred. No. 0;				
Matches 2195; Conservative	0; Mismatches	0; Indels	0; Gaps	0;	
Oy	1	AATCGAAAGTTTGACCGTTTTCAGCTCTACTACATATAGGAACTGTGCT	60		
Db	1	AATCGAAAGTTTGACCGTTTTCAGCTCTACTACATATAGGAACTGTGCT	60		
Oy	61	AAATATAATGAGACCTTATATATGTCGCTGATTAATGAATTAAGTGTGCT	120		
Db	61	AAATATAATGAGACCTTATATATGTCGCTGATTAATGAATTAAGTGTGCT	120		
Oy	121	CATCACCTACTTTTGTGCAATCGGCTAATATAAAGAGTGCCTACAGTTTGT	180		
Db	121	CATCACCTACTTTTGTGCAATCGGCTAATATAAAGAGTGCCTACAGTTTGT	180		
Oy	181	TTTCCTAGTATATTAAGTGGGAAATGAATCATTTATGCTTAGAATACGTTGATC	240		

181 |TTTCTTAAATTAAGTGGGAAAATGAATCATTAATGCTTAAGATATACCTTCATC| 240  
QY 241 |TCTGTCATGAAGTTAAATTAATTCGAGTAGCCATTAATTCATCAACTCTCTTGATA| 300  
DB 241 |TCTGTCATGAAGTTAAATTAATTCGAGTAGCCATTAATTCATCAACTCTCTTGATA| 300  
QY 301 |AAAAAATCTTCTAGCTGAATCTCAATGGGTAAAGAGATATTTTTTTTTAAAAAAT| 360  
DB 301 |AAAAAATCTTCTAGCTGAATCTCAATGGGTAAAGAGATATTTTTTTTTAAAAAAT| 360  
QY 361 |AGAAATGAATATTCGAAAGTATCGGCAAAAGTTTAAACATTAATTAATTAATTTAT| 420  
DB 361 |AGAAATGAATATTCGAAAGTATCGGCAAAAGTTTAAACATTAATTAATTAATTTAT| 420  
QY 421 |AGTTTGTGATTCGTATATCGCAGCTCATTAAGACATGTCCTTACATCTCAATTT| 480  
DB 421 |AGTTTGTGATTCGTATATTCGCAAGTCATTAAGACATGTCCTTACATCTCAATTT| 480  
QY 481 |TATTTAGTAATTAAGACAATGACTTAATTTTTATTTATCTTTTTCGATTAGATGC| 540  
DB 481 |TATTTAGTAATTAAGACAATGACTTAATTTTTATTTATCTTTTTCGATTAGATGC| 540  
QY 541 |AAGGTAATTAAGACAATGACTTTGTCTCATGTCAGTGTGAGTGCACCTCTCATAC| 600  
DB 541 |AAGGTAATTAAGACAATGACTTTGTCTCATGTCAGTGTGAGTGCACCTCTCATAC| 600  
QY 601 |GTTCAACTAGCGACATCTCCAAATATCACTGCGCTATTTAATTAATTAATTAAT| 660  
DB 601 |GTTCAACTAGCGACATCTCCAAATATCACTGCGCTATTTAATTAATTAATTAAT| 660  
QY 661 |TCTGAATTAAGACAATGACTTACACATCACAGACCACTTTAATAATATCTAAAT| 720  
DB 661 |TCTGAATTAAGACAATGACTTACACATCACAGACCACTTTAATAATATCTAAAT| 720  
QY 721 |ATTAATTTACAGATTAAGCAATGAAGATGAAGAAAGCAATTTAGTTTTCATACAA| 780  
DB 721 |ATTAATTTACAGATTAAGCAATGAAGATGAAGAAAGCAATTTAGTTTTCATACAA| 780  
QY 781 |AAAAAAGAAATTTTGTCTGTGCGGAGGCGCAATCTCCATATTTGGGACACAGGCA| 840  
DB 781 |AAAAAAGAAATTTTGTCTGTGCGGAGGCGCAATCTCCATATTTGGGACACAGGCA| 840  
QY 841 |CAACAGATGTGCTGCCACAGAACCAACCAAAAAAGATATCTAACGAGAGACAGA| 900  
DB 841 |CAACAGATGTGCTGCCACAGAACCAACCAAAAAAGATATCTAACGAGAGACAGA| 900  
QY 901 |AGTCCGCAACACTTTTAAACAGCAGGCTTTGCGGCAGAGAGAGAGAGAGGCAAG| 960  
DB 901 |AGTCCGCAACACTTTTAAACAGCAGGCTTTGCGGCAGAGAGAGAGAGAGGCAAG| 960  
QY 961 |AAAAACAAGCATCTCTCTCCCATCTAATAATCTCCGCCCTTTTCCCTCTCTATA| 1020  
DB 961 |AAAAACAAGCATCTCTCTCCCATCTAATAATCTCCGCCCTTTTCCCTCTCTATA| 1020  
QY 1021 |TAGAGGCAATCCAGGCAAGAGAGAGAGAGACCAAGACACGCACTTAGCAAGCCG| 1080  
DB 1021 |TAGAGGCAATCCAGGCAAGAGAGAGAGAGACCAAGACACGCACTTAGCAAGCCG| 1080  
QY 1081 |AGCGACCGCTTCTGATCCATATCTTCGGTCGATCTCTTGTCGATCTCTCCCTCC| 1140  
DB 1081 |AGCGACCGCTTCTGATCCATATCTTCGGTCGATCTCTTGTCGATCTCTCCCTCC| 1140  
QY 1141 |TCACCTCTCTCCACAGGGAATGAGCCCTGGGTTCTTGGATTTATGTTCTAGGT| 1200  
DB 1141 |TCACCTCTCTCCACAGGGAATGAGCCCTGGGTTCTTGGATTTATGTTCTAGGT| 1200  
QY 1201 |TGTGTAGTACGGGCGTTGTAGTTAGGAAAGGGATCTGTATCTGTGATATCTGTTCT| 1260  
DB 1201 |TGTGTAGTACGGGCGTTGTAGTTAGGAAAGGGATCTGTATCTGTGATATCTGTTCT| 1260  
QY 1261 |TGGATTTGGGATAGAGGGGTTCTTGATGTTGCAATGTTATCGTTTGGTTGATAGT| 1320  
DB 1261 |TGGATTTGGGATAGAGGGGTTCTTGATGTTGCAATGTTATCGTTTGGTTGATAGT| 1320

DB 1261 |TGGATTTGGGATAGAGGGGTTCTTGATGTTGCAATGTTATCGTTTGGTTGATAGT| 1320  
QY 1321 |ATGTTTTCAATCGTCTGAGAGCTCTATGGAATGAATGTTAGGTTACGAACTT| 1380  
DB 1321 |ATGTTTTCAATCGTCTGAGAGCTCTATGGAATGAATGTTAGGTTACGAACTT| 1380  
QY 1381 |GGGATTTTGTAGTACCTTTTGTGTGAGTTAAATCAGAGCACCGGTATTTTGTGCT| 1440  
DB 1381 |GGGATTTTGTAGTACCTTTTGTGTGAGTTAAATCAGAGCACCGGTATTTTGTGCT| 1440  
QY 1441 |GTAATTAAGTAATGATTTGTTGCTCGATTTCTGTAGTATGCTTCTCATTTGACGA| 1500  
DB 1441 |GTAATTAAGTAATGATTTGTTGCTCGATTTCTGTAGTATGCTTCTCATTTGACGA| 1500  
QY 1501 |AGCTATCCTTTGTTATTCCTATTAAGCAAAATATCAACTTTGAAAGCGTCCGT| 1560  
DB 1501 |AGCTATCCTTTGTTATTCCTATTAAGCAAAATATCAACTTTGAAAGCGTCCGT| 1560  
QY 1561 |TGATGAGATTAATGATTTGTTTACGCTGTCCAAATTTTCCGAGCTGGCTTTAG| 1620  
DB 1561 |TGATGAGATTAATGATTTGTTTACGCTGTCCAAATTTTCCGAGCTGGCTTTAG| 1620  
QY 1621 |ATACAGTAGTCCCATCAAGAAATTCATGAAGAGTTATATCTCAGAGACAGGGAT| 1680  
DB 1621 |ATACAGTAGTCCCATCAAGAAATTCATGAAGAGTTATATCTCAGAGACAGGGAT| 1680  
QY 1681 |TCCCTGTTCTTCCGATTTGCTTATGCTCCAGAAATTTTCCCAATATCTTAAAGT| 1740  
DB 1681 |TCCCTGTTCTTCCGATTTGCTTATGCTCCAGAAATTTTCCCAATATCTTAAAGT| 1740  
QY 1741 |CACTTTCGTTGCTCAATGAATTTGATTTGCTCAAAATATGCTTTATAGCTTATCC| 1800  
DB 1741 |CACTTTCGTTGCTCAATGAATTTGATTTGCTCAAAATATGCTTTATAGCTTATCC| 1800  
QY 1801 |TAGCTGATGTTCAATTTTATGAGTAATACCCCTATAGTTAGTACAGAGAACTTATCC| 1860  
DB 1801 |TAGCTGATGTTCAATTTTATGAGTAATACCCCTATAGTTAGTACAGAGAACTTATCC| 1860  
QY 1861 |GATTTCTGATCTCCATTTTATTAATTAATGAATGAACGTAGACATTAACATTTAT| 1920  
DB 1861 |GATTTCTGATCTCCATTTTATTAATTAATGAATGAACGTAGACATTAACATTTAT| 1920  
QY 1921 |GGATTAATTTTATTAATGCTTTACCCCTTCAATTTCTGAGCTGAAGTCTGGCATGA| 1980  
DB 1921 |GGATTAATTTTATTAATGCTTTACCCCTTCAATTTCTGAGCTGAAGTCTGGCATGA| 1980  
QY 1981 |ACTGTCCTCAATTTGTTTGAATTAATGAATGAACGTAGATTAATCTGCTGTATTC| 2040  
DB 1981 |ACTGTCCTCAATTTGTTTGAATTAATGAATGAACGTAGATTAATCTGCTGTATTC| 2040  
QY 2041 |TACCTGTAGAAATTTTGTGTTATCTTGAATCTGCTGTATTAACAGAAAGAAATTTAT| 2100  
DB 2041 |TACCTGTAGAAATTTTGTGTTATCTTGAATCTGCTGTATTAACAGAAAGAAATTTAT| 2100  
QY 2101 |GAAGCTGTAAATCGGAGATGTTATACCTGTTCTGTATGATTAATTTCTTTGTCAGTT| 2160  
DB 2101 |GAAGCTGTAAATCGGAGATGTTATACCTGTTCTGTATGATTAATTTCTTTGTCAGTT| 2160  
QY 2161 |CTTGTGTAGCTTGCACTTTACACAGCAAGTTTC| 2195  
DB 2161 |CTTGTGTAGCTTGCACTTTACACAGCAAGTTTC| 2195

RESULT 2  
BD251965/C 9361 bp DNA linear PAT 17-JUL-2003  
LOCUS BD251965 Artificial matrix attachment region for increasing expression of  
DEFINITION genes introduced in plant cells.  
ACCESSION BD251965  
VERSION BD251965.1 GI:33061735  
KEYWORDS JP 2002531097-A/27.  
SOURCE synthetic construct  
ORGANISM synthetic construct

other sequences; artificial sequences.  
1 (bases 1 to 9361)  
Geest,A.H.V.D., Ainley,M.W., Cowen,N.M., Welter,M.E. and  
Woosley,A.T.  
Artificial matrix attachment region for increasing expression of  
genes introduced in plant cells  
Patent: JP 2002531097-A 27 24-SEP-2002;  
DOM AGROSCIENCES LLC  
OS Artificial Sequence  
PN JP 2002531097-A/27  
PD 24-SEP-2002  
PP 30-NOV-1999 JP 2000585431  
PR 01-DEC-1998 US 60/110437  
PI APOLOJIA HM VAN DER GEBST, MICHAEL W AINLEY, NEIL M COWEN, MARY E  
WELTER.  
PI AARON T WOOSLEY  
PC C12N15/09,A01H5/00,C12N5/10,C12N15/00,C12N5/00 CC  
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FT location/Qualifiers  
Location/Qualifiers  
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/db\_xref="taxon:32630"

ORIGIN

Query Match	57.7%; Score 1267; DB 6; Length 9361;
Best Local Similarity	99.6%; Pred. No. 0;
Matches 1567; Conservative	0; Mismatches 6; Indels 0; Gaps 0;
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DB 6472 AATATACGCGCTATTTAATTAAGTACCATATCTGAATTCAGACACTTACCA 6413	DB 5872 TAGAAGGGGATCTGTATCTGTATGATTCCTGTTCTTGATTTGGGATAGAGGGCTTC 5813
QY 683 TCACGAGACCACTTTAATATATCTAAATACAAAATTAATTTTACAGATAGCATGA 742	QY 1283 TTGATCTGCATGTTATCGGTCCGGTTGATAGTATGATTTTCAATCGCTGGAGA 1342
DB 6412 TCACGAGACCACTTTAATATATCTAAATACAAAATTAATTTTACAGATAGCATGA 6353	DB 5812 TTGATCTGCATGTTATCGGTCCGGTTGATAGTATGATTTTCAATCGCTGGAGA 5753
QY 743 AAGATGAAACGAATATTTAGTTTTCATACATAAAAAAATTTTGTCTCGT 802	QY 1343 GCTATGAAATGAATATGTTTAGGGTACGGAATCTTGCGATTTTGTAGTACCTTTTG 1402
DB 6352 AAGATGAAACGAATATTTAGTTTTCATACATAAAAAAATTTTGTCTCGT 6293	DB 5752 GCTATGAAATGAATATGTTTAGGGTACGGAATCTTGCGATTTTGTAGTACCTTTTG 5693
QY 803 GCGCGAGCGCATCTCCATATTTGGGACACAGGCAACAGATGGTGGCCACAGA 862	QY 1403 TTGAGTAAATACAGACACCGGGATTTTGGTCTGTGTATTAATAAGTACATTTGTTTG 1462
DB 6292 GCGCGAGCGCATCTCCATATTTGGGACACAGGCAACAGATGGTGGCCACAGA 6233	DB 5692 TTGAGTAAATACAGACACCGGGATTTTGGTCTGTGTATTAATAAGTACATTTGTTTG 5633
QY 863 ACAACCCACAAAACGATGATCTAAGCGAGGACAGCAAGTCCGCAACACTTTTAA 922	QY 1463 GTCTCGATTCGTGTAGTATGATTCCTGATTTTGACGAAGCTATCTTGTATTCCTT 1522
DB 6232 ACAACCCACAAAACGATGATCTAAGCGAGGACAGCAAGTCCGCAACACTTTTAA 6173	DB 5632 GTCTCGATTCGTGTAGTATGATTCCTGATTTTGACGAAGCTATCTTGTATTCCTT 5573
QY 923 GCAGGCTTTGCGCCAGAGAGAGAGAGGCAAAAGAAACCAAGCATCTCTCTC 982	QY 1523 ATTGAACAAAATTAATCCAACTTTGAGAAGCGTCCGTTGATGAGATTTGAATGATTT 1582
DB 6172 GCAGGCTTTGCGCCAGAGAGAGAGAGGCAAAAGAAACCAAGCATCTCTCTC 6113	DB 5572 ATTGAACAAAATTAATCCAACTTTGAGAAGCGTCCGTTGATGAGATTTGAATGATTT 5513
QY 983 CCATCTAATAATTCCTCCCTTTTCCCTCTCTATATAGAGGCGATCCAAGCAAGAA 1042	QY 1583 CTTAAGCCTGTCCAAAATTTGCGACGCTGGCTTTGATGATACAGTATGCCATACGAA 1642
DB 6112 CCATCTAATAATTCCTCCCTTTTCCCTCTCTATATAGAGGCGATCCAAGCAAGAA 6053	DB 5512 CTTAAGCCTGTCCAAAATTTGCGACGCTGGCTTTGATGATACAGTATGCCATACGAA 5453
QY 1043 GAGGAGAGACCAAGGACACGGAAGTGAAGAGGCGAGCGGCTTTCTTGATCCA 1102	QY 1643 ATTCAATGAAACAGTATTAATCTTCAAGAACGGGATTTCCCTGTTCCGATTTGCTT 1702
DB 6052 GAGGAGAGACCAAGGACACGGAAGTGAAGAGGCGAGCGGCTTTCTTGATCCA 5993	QY 5452 ATTCAATGAAACAGTATTAATCTTCAAGAACGGGATTTCCCTGTTCCGATTTGCTT 5393
QY 1103 TATCTTCGCGTCGATGTTCTGTGATCTCTCTCTCTCTCACTCTCTCAAGGGTA 1162	QY 1703 TAGTCCAGAAATTTTTTCCCAATATCTTAAAGTCACTTTCGTTCAAGTCAATG 1762
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QY 1163 TGTGCGCTTGGTTGTTCTTGATTTATTTGTTAGGTTGTGTAGTACGGGCGTTGATGT 1222	QY 1762 AATGATGCTCAAAATAATGCTTTTATAGCTTATCTAGCTGTATGATTCAGTTATAG 1822
DB 5932 TGTGCGCTTGGTTGTTCTTGATTTATTTGTTAGGTTGTGTAGTACGGGCGTTGATGT 5873	QY 5332 AATGATGCTCAAAATAATGCTTTTATAGCTTATCTAGCTGTATGATTCAGTTATAG 5273

QY 1223 TAGAAGGGGATCTGTATCTGTATGATTCCTGTTCTTGATTTGGGATAGAGGGCTTC 1282	QY 1762 AATGATGCTCAAAATAATGCTTTTATAGCTTATCTAGCTGTATGATTCAGTTATAG 1822
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DB 5812 TTGATCTGCATGTTATCGGTCCGGTTGATAGTATGATTTTCAATCGCTGGAGA 5753	QY 5272 TTAATCCCTATATGTTTATGTCAGAGAGAACTTATCCGATTTTCGATCTCCATTTTAA 5213
QY 1343 GCTATGAAATGAATATGTTTAGGGTACGGAATCTTGCGATTTTGTAGTACCTTTTG 1402	QY 1883 TTAATGAAATGAACGTGATGATTAAGAGTATCTTGGATTTATTTTATATAGCTT 1942
DB 5752 GCTATGAAATGAATATGTTTAGGGTACGGAATCTTGCGATTTTGTAGTACCTTTTG 5693	QY 5212 TTAATGAAATGAACGTGATGATTAAGAGTATCTTGGATTTATTTTATATAGCTT 5153
QY 1403 TTGAGTAAATACAGACACCGGGATTTTGGTCTGTGTATTAATAAGTACATTTGTTTG 1462	QY 1943 TCACCCCTTCATTTATCTGAGCTGAAGTCTGGCATGAACGTGCTCAATTTTGTTCGA 2002
DB 5692 TTGAGTAAATACAGACACCGGGATTTTGGTCTGTGTATTAATAAGTACATTTGTTTG 5633	DB 5152 TCACCCCTTCATTTATCTGAGCTGAAGTCTGGCATGAACGTGCTCAATTTTGTTCGA 5093
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DB 5632 GTCTCGATTCGTGTAGTATGATTCCTGATTTTGACGAAGCTATCTTGTATTCCTT 5573	DB 5092 AATTCATGATGATTAATCTATGATTAATCTCTGTATATCTACTGTGAAAGTTCTTTTGG 5033
QY 1523 ATTGAACAAAATTAATCCAACTTTGAGAAGCGTCCGTTGATGAGATTTGAATGATTT 1582	QY 2063 GTTATTCCTGACGCTGATTAACAGAAAGAAATTTATGAGCTGTAATCGGGATAGTTA 2122
DB 5572 ATTGAACAAAATTAATCCAACTTTGAGAAGCGTCCGTTGATGAGATTTGAATGATTT 5513	DB 5032 GTTATTCCTGACGCTGATTAACAGAAAGAAATTTATGAGCTGTAATCGGGATAGTTA 4973
QY 1583 CTTAAGCCTGTCCAAAATTTGCGACGCTGGCTTTGATGATACAGTATGCCATACGAA 1642	QY 2123 TACTGCTGTTCTTATGATTCATTTCTTGTGCAAGTCTTGGTATGAGCTTCCACTTTC 2182
DB 5512 CTTAAGCCTGTCCAAAATTTGCGACGCTGGCTTTGATGATACAGTATGCCATACGAA 5453	DB 4972 TACTGCTGTTCTTATGATTCATTTCTTGTGCAAGTCTTGGTATGAGCTTCCACTTTC 4913
QY 1643 ATTCAATGAAACAGTATTAATCTTCAAGAACGGGATTTCCCTGTTCCGATTTGCTT 1702	QY 2183 ACCAGCAAGTTC 2195
QY 5452 ATTCAATGAAACAGTATTAATCTTCAAGAACGGGATTTCCCTGTTCCGATTTGCTT 5393	DB 4912 ACCAGCAAGTTC 4900
QY 1703 TAGTCCAGAAATTTTTTCCCAATATCTTAAAGTCACTTTCGTTCAAGTCAATG 1762	
QY 5392 TAGTCCAGAAATTTTTTCCCAATATCTTAAAGTCACTTTCGTTCAAGTCAATG 5333	
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QY 5332 AATGATGCTCAAAATAATGCTTTTATAGCTTATCTAGCTGTATGATTCAGTTATAG 5273	
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QY 5272 TTAATCCCTATATGTTTATGTCAGAGAGAACTTATCCGATTTTCGATCTCCATTTTAA 5213	
QY 1883 TTAATGAAATGAACGTGATGATTAAGAGTATCTTGGATTTATTTTATATAGCTT 1942	
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DB 5152 TCACCCCTTCATTTATCTGAGCTGAAGTCTGGCATGAACGTGCTCAATTTTGTTCGA 5093	
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DB 5032 GTTATTCCTGACGCTGATTAACAGAAAGAAATTTATGAGCTGTAATCGGGATAGTTA 4973	
QY 2123 TACTGCTGTTCTTATGATTCATTTCTTGTGCAAGTCTTGGTATGAGCTTCCACTTTC 2182	
DB 4972 TACTGCTGTTCTTATGATTCATTTCTTGTGCAAGTCTTGGTATGAGCTTCCACTTTC 4913	
QY 2183 ACCAGCAAGTTC 2195	
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RESULT 3  
BD251966/c BD251966 10629 bp DNA linear PART 17-UTL-2003  
LOCUS  
DEFINITION Artificial matrix attachment region for increasing expression of

genes introduced in plant cells.  
BD251966  
BD251966.1 GI:33061736  
JP 2002531097-A/28.  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1 (bases 1 to 10629)  
Geest,A.H.V.D., Ainley,M.W., Cowen,N.M., Welter,M.E. and  
Woosley,A.T.  
AUTHORS  
TITLE  
Artificial matrix attachment region for increasing expression of  
genes introduced in plant cells  
JOURNAL  
Patent: JP 2002531097-A 28 24-SEP-2002;  
COMMENT  
DOW AGROSCIENCES LLC  
OS Artificial Sequence  
PN JP 2002531097-A/28  
PD 24-SEP-2002  
PF 30-NOV-1999 JP 2000585431  
PR 01-DEC-1998 US 60/110437  
PI APOLO니아 HM VAN DER GEBST,MICHAEL W AINLEY,NEIL M COWEN,MARY E  
PI WELTER,  
PI AARON T WOOSLEY  
PC C12N15/09,A01H5/00,C12N5/10,C12N15/00,C12N5/00 CC  
Description of Artificial Sequence:patGOS2At-hpt FH Key  
Location/Qualifiers  
FT source 1..10629  
FT Location/Qualifiers  
1..10629  
/organism="synthetic construct"  
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Query Match 57.7%; Score 1267; DB 6; Length 10629;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1567; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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623 AATTATCACTCGGCTATTTAATCACTTAGTAGTGCATATCTGAATTCAGACCTTCACCA 682  
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Db 7051 TCACGAGACCACTTTTAATATATCTAAATAACAATAATTTTACAGATAGCATGA 6992  
Qy 743 AAAGTATGAACGAACTATTAGTTTTCACATACAAAAAAGAAATTTTGTCTGT 802  
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Qy 983 CCATCTATAATTTCCCTCCCCCTTTTCCCTCTCTATATAGAGGATCCAGCCAAAGA 1042  
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631 TATCTTCGGGTGAGGTTCTTTGGTGCATCTCTTCCCTCTCCACTCTCTCAAGGATA 6572  
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Qy 1943 TCACCCCTCATTTATCTGAGCTGAAGTCTGGCATGATAGTCTCTCAATTTTGTTC 2002  
Db 5791 TCACCCCTCATTTATCTGAGCTGAAGTCTGGCATGATAGTCTCTCAATTTTGTTC 5732  
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Db 5611 TACTGCTTGTCTTATGATTCATTTCTTTGTGAGATTTCTTGTTAGCTTGGCACTTTC 5552  
Qy 2183 ACCAGCAAGTTC 2195  
Db 5551 ACCAGCAAGTTC 5539



RESULT 4  
LOCUS AF294979 14203 bp DNA circular SYN 24-MAY-2002  
DEFINITION Binary vector PINDEX1, complete sequence.  
ACCESSION AF294979  
VERSION AF294979.1 GI:11559663  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLES  
JOURNAL  
PUBMED  
REFERENCE  
2 (bases 1 to 14203)  
Ouwkerk, P.B., de Kam, R.J., Hoge, J.H. and Meijer, A.H.  
Glucocorticoid-inducible gene expression in rice  
Planta 213 (3), 370-378 (2001)  
11506359  
2 (bases 1 to 14203)  
Ouwkerk, P.B.,  
Direct Submission  
Submitted (11-AUG-2000) Dept. of Molecular Cell Biology, Institute  
for Molecular Plant Sciences, Wassenaarseweg 64, Leiden 2333 AL,  
Netherlands  
PINDEX1 is a binary vector designed for glucocorticoid-inducible  
gene expression in plants and is optimized for use in rice; PINDEX1  
is part of a series of four PINDEX vectors (Genbank Accession  
Numbers AF294979-AF294982). PINDEX vectors are based on parts of  
pCAMBIA-1300 encoded by Genbank Accession Number AF234296 and  
pTA1002 (Koyama, T. and Chua N.-H., 1997, Plant J. 11:605-612).  
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4357..4427  
/note="contains 4 upstream activation sites; tetramer of  
the GVG binding site"  
4474..4531  
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4548..4583  
misc\_feature

/note="multiple cloning site; contains unique restriction  
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VERSION AF294980.1 GI:11559666  
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1 (bases 1 to 14230)  
Ouwkerk, P.B., de Kam, R.J., Hoge, J.H. and Meijer, A.H.  
Glucocorticoid-inducible gene expression in rice  
Planta 213 (3), 370-378 (2001)  
PUBMED 11506359  
REFERENCE  
2 (bases 1 to 14230)  
Ouwkerk, P.B.P.  
TITLE Direct Submission  
JOURNAL Submitted (11-AUG-2000) Dept. of Molecular Cell Biology, Institute for Molecular Plant Sciences, Wageningen 64, Leiden 2333 AL, Netherlands

COMMENT  
pINDEX2 is a binary vector designed for glucocorticoid-inducible gene expression in plants and is optimized for use in rice; pINDEX2 is part of a series of four pINDEX vectors (Genbank Accession Numbers AF294979-AF294982). pINDEX vectors are based on parts of pCAMBIA-1300 encoded by Genbank Accession Number AF234296 and pTA7002 (Novena, T. and Chua N.-H., 1997, Plant J. 11:605-612).

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 ORGANISM Oryza sativa (japonica cultivar-group)  
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 REFERENCE  
 1 Sasaki, T., Matsumoto, T. and Yamamoto, K.  
 Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC  
 clone: OUI365\_D04  
 JOURNAL Published Only in Database (2001)  
 2 (bases 1 to 105692)  
 AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-JUL-2001) Takuji Sasaki, National Institute of  
 Agrobiological Resources, Rice Genome Research Program, Kannondai  
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
 (E-mail: tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/  
 Tel: 81-298-38-7441, Fax: 81-298-38-7468)  
 The nucleotide sequence of this BAC clone was generated by  
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 COMMENT  
 NOTE: It currently consists of 1 contigs. Gaps between the contigs  
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 to be correct as given, however the sizes of the gaps between them  
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 sequence will be replaced by the finished sequence as soon as it is  
 available and the accession number will be preserved.  
 \* NOTE: This is a 'working draft' sequence.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
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 LOCUS Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 7,  
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 ACCESSION AP004674  
 VERSION AP004674.2 GI:26017274  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
 AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.  
 TITLE Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC  
 clone: P0681F05  
 JOURNAL Published Only in Database (2002)  
 AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.  
 TITLE Direct Submision  
 JOURNAL Submitted (23-JAN-2002) Takuji Sasaki, National Institute of  
 Agricultural Sciences, Rice Genome Research Program, Kannondai  
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
 (E-mail: tsasak@affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/  
 Tel: 81-298-38-7441, Fax: 81-298-38-7468)  
 On Dec 3, 2002 this sequence version replaced gi:18307752.  
 Gene were predicted from the integrated results of the following:  
 GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), GENESH  
 (http://www.softberry.com/), GeneMark.hmm  
 (http://opal.biology.gatech.edu/GeneMark/), Glimmer

## FEATURES

## source

(http://www.tigr.org/tdb/glimmer/glar\_form.html), RicheHM  
 (http://rgp.dna.affrc.go.jp/RiceHM/), SplinePredictor  
 (http://bioinformatics.lasstate.edu/cgi-bin/sp.cgi), sim4  
 (http://globin.cse.psu.edu/html/docs/sim.html), gapp2  
 (http://www.tigr.org/software/glimmer/). BLASTN and BLASTX. The  
 genomic sequence was searched against NCBI Nonredundant Protein  
 database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA  
 sequence database at RGP or DBJ. Protein homologs of the coding  
 regions were searched against NCBI Nonredundant Protein database  
 with BLASTP. ESTs represent the identified cDNA sequences using  
 BLASTN with the corresponding DBJ accession no. and RGP clone ID.  
 Full-length cDNAs represent the identified cDNA sequences using  
 BLASTN with the corresponding DBJ accession no.  
 A gene with identity or significant homology to a protein is  
 classified based on the protein name to indicate the homology level  
 such as same name, 'putative', and '-like protein'. A gene without  
 significant homology to any protein but with full-length cDNA or  
 EST homology (covering almost the entire length of partial  
 sequence) is classified as an 'unknown' protein. A gene predicted  
 by two or more gene prediction programs is classified as a  
 'hypothetical' protein according to IRGSP standard. A gene  
 predicted by a single gene prediction program is also classified as  
 a probable 'hypothetical' protein and is included as a  
 miscellaneous feature of the sequence.  
 The orientation of the sequence is from T7 to SP6 of the PAC clone.  
 This sequence of P0681F05 clone has an overlap with OSJNB0007H12  
 (DBJ: AP004990) clone at 5' end and with OSJNB0044C15 (DBJ:  
 AP005850) at 3' end. Detailed information on overlap and assembly  
 quality together with annotation of this entry is available at  
 http://rgp.dna.affrc.go.jp/Genomeseg.html.

## Location/Qualifiers

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gene	pseudo 19824..20405 /gene="P0681F05.105" join(<19824..19909,20071..20178,20294..>20405) /gene="P0681F05.105" /note="start and end point are not identified" join(19824..19909,20071..20178,20294..20405) /gene="P0681F05.105" /note="predicted by Genemark.hmm etc."
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gene	complement(join(27163..27332,27442..27529))

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VERSION CQ895917.1 GI:55467905  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1 sanz Molinero, A.I.  
AUTHORS  
TITLE  
Plants having modified growth characteristics and method for making  
the same  
JOURNAL Patent: WO 2004090142-A 7 21-OCT-2004;  
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DB 1281 TTGATGTTCAATGTTATCGGTTGAGTGTGATTAAGTATGATGATGATGATGATGATGAT 1340  
QY 1343 GCTCTATGAAATGAAATGTTTAAAGGTACGAAATCTTGGATTTGTAGTACCTTTTG 1402  
DB 1341 GCTCTATGAAATGAAATGTTTAAAGGTACGAAATCTTGGATTTGTAGTACCTTTTG 1400  
QY 1403 TTTGAGGTAAATCAGAGACCGGTGATTTTGGTGTGATTAAGTATGATGATGATGATGATGAT 1462  
DB 1401 TTTGAGGTAAATCAGAGACCGGTGATTTTGGTGTGATTAAGTATGATGATGATGATGATGAT 1460  
QY 1463 GTCTCGATTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1522  
DB 1461 GTCTCGATTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1520  
QY 1523 ATTGAACAAAAATATCAACTTGAAGCGTCCGTTGATGATGATGATGATGATGATGAT 1582  
DB 1521 ATTGAACAAAAATATCAACTTGAAGCGTCCGTTGATGATGATGATGATGATGATGAT 1580  
QY 1583 CTTAAGCCCTGCAAAATTTGAGCTGCTGTTAGTATAGTATAGTATAGTATAGTATAGTAT 1642  
DB 1581 CTTAAGCCCTGCAAAATTTGAGCTGCTGTTAGTATAGTATAGTATAGTATAGTATAGTAT 1640  
QY 1643 ATTCATGAAAACATTAATATCTCAGAACAGGGGATTCCTGTTCTTCGATTTGCTT 1702  
DB 1641 ATTCATGAAAACATTAATATCTCAGAACAGGGGATTCCTGTTCTTCGATTTGCTT 1700  
QY 1703 TAGTCCAGAAATTTTTTCCCAAAATATCTTAAAAAGTCACTTTCGTTCAAGTTCAATG 1762  
DB 1701 TAGTCCAGAAATTTTTTCCCAAAATATCTTAAAAAGTCACTTTCGTTCAAGTTCAATG 1760  
QY 1763 AATTGATGCTCAAAATATATGCTTTATAGCTTATAGCTTATAGCTTATAGCTTATAGCT 1822  
DB 1761 AATTGATGCTCAAAATATATGCTTTATAGCTTATAGCTTATAGCTTATAGCTTATAGCT 1820  
QY 1823 TAAATACCCCTATAGTTTATGTCAGAGAAAGAACTTATCCGATTTGATCTCATTTTAA 1882  
DB 1821 TAAATACCCCTATAGTTTATGTCAGAGAAAGAACTTATCCGATTTGATCTCATTTTAA 1880  
QY 1883 TTAATATGAATGAATGATGATTAAGCAATTAAGCAATTAATTTTATTTTATAGCTT 1942

DB 1881 TTAATATGAATGAATGATGATTAAGCAATTAAGCAATTAATTTTATTTTATAGCTC 1940  
QY 1943 TCACCCCTTCATTAATTCAGAGCTGAAGCTGCGCATGAATCTGCTCAATTTTGTTC 2002  
DB 1941 TCACCCCTTCATTAATTCAGAGCTGAAGCTGCGCATGAATCTGCTCAATTTTGTTC 2000  
QY 2003 AATTACATTCGATTAATCTATGATTAATCTCTTGTGATTAACCTGTAGAAATTTCTTTTG 2062  
DB 2001 AATTACATTCGATTAATCTATGATTAATCTCTTGTGATTAACCTGTAGAAATTTCTTTTG 2060  
QY 2063 GTTATTCCTGACCTGCTGATTAAGAAAGAAATTTATGAAGCTGTAATCGGATAGTTA 2122  
DB 2061 GTTATTCCTGACCTGCTGATTAAGAAAGAAATTTATGAAGCTGTAATCGGATAGTTA 2120  
QY 2123 TACTGCTTGTCTTAATGATTAATTCCTTGTGACAGTTCTTGTGTAGCTTGCACCTTTC 2182  
DB 2121 TACTGCTTGTCTTAATGATTAATTCCTTGTGACAGTTCTTGTGTAGCTTGCACCTTTC 2180  
QY 2183 ACCAGCAAAAGTTC 2195  
DB 2181 ACCAGCAAAAGTTC 2193

RESULT 11  
CS055056 2191 bp DNA linear PAT 31-MAR-2005  
LOCUS CS055056  
DEFINITION Sequence 15 from Patent WO2005024029.  
ACCESSION CS055056  
VERSION CS055056.1 GI:62121528  
KEYWORDS

SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehmerioideae; Oryzaceae; Oryza.

REFERENCE  
1 Broekaert, W., Frankard, V., Hatzfeld, Y. and Mitronov, V.  
AUTHORS  
Plants having modified growth characteristics and method for making  
the same  
JOURNAL Patent: WO 2005024029-A 15 17-MAR-2005;  
CropDesign N.V. (BE)

FEATURES  
source  
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Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:4530"

ORIGIN  
Query Match 42.6%; Score 936; DB 6; Length 2191;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1306; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 623 AATATCACTGCGCTAATTAATCACTTAATGAGAGAAATTCGAATTCAGAGCACTTCACCA 682  
DB 621 AATATCACTGCGCTAATTAATCACTTAATGAGAGAAATTCGAATTCAGAGCACTTCACCA 680  
QY 683 TCACAGAGCACTTTAATATCTAAATATACAAAAAATTAATTTTACAGAAATGACATGA 742  
DB 681 TCACAGAGCACTTTAATATCTAAATATACAAAAAATTAATTTTACAGAAATGACATGA 740  
QY 743 AAAGTATGAACGAATTAATTTAGGTTTTCATATACAAAAAAGAAATTTTGTCTGT 802  
DB 741 AAAGTATGAACGAATTAATTTAGGTTTTCATATACAAAAAAGAAATTTTGTCTGT 800  
QY 803 GCGGAGGCGCAATCTCCCATATTTGGGCAACAGGCAACAAAGATGGCTGCCACAGA 862  
DB 801 GCGGAGGCGCAATCTCCCATATTTGGGCAACAGGCAACAAAGATGGCTGCCACAGA 860  
QY 863 ACNACCCACAAAAAGATGATCTTAACGAG 922  
DB 861 ACNACCCACAAAAAGATGATCTTAACGAG 920

QY	923	GCAGGCTTTGGGCGACGAGAGAGGAGGACCAAAAAACCAAGATCTCTCCTC	982
Db	921	GCAGGCTTTGGGCGACGAGAGAGGAGGACCAAAAAACCAAGATCTCTCCTC	980
QY	983	CCATCTATAAATTCCTCCCTCTTCCCTCTCTATATAGAGGCATCCAGCCAA	1042
Db	981	CCATCTATAAATTCCTCCCTCTTCCCTCTCTATATAGAGGCATCCAGCCAA	1040
QY	1043	GAGGAGAGGACCAAGGACAGGCCACTAGCAGAAAGCCGAGATCCGTTCGAT	1102
Db	1041	GAGGAGAGGACCAAGGACAGGCCACTAGCAGAAAGCCGAGATCCGTTCGAT	1100
QY	1103	TATCTTCGGGTCGAGTCTTGGTGCATCTTCCCTCCCTCCAGCCCTCTCAGAG	1162
Db	1101	TATCTTCGGGTCGAGTCTTGGTGCATCTTCCCTCCCTCCAGCCCTCTCAGAG	1160
QY	1163	TGTGCGCTTCGGTGTGTTCTTGGAATTAATGTCTAGTGTGTAGTACGGCGT	1222
Db	1161	TGTGCGCTTCGGTGTGTTCTTGGAATTAATGTCTAGTGTGTAGTACGGCGT	1220
QY	1223	TAGGAAAGGGGATCTGTATCTGTATGATTCCTGTTCTTGGATTTGGAGGGT	1282
Db	1221	TAGGAAAGGGGATCTGTATCTGTATGATTCCTGTTCTTGGATTTGGAGGGT	1280
QY	1283	TTGATGTTCGATGATTCGGTTCGGTTCGATTTAGATGATGCTTCAATGTC	1342
Db	1281	TTGATGTTCGATGATTCGGTTCGGTTCGATTTAGATGATGCTTCAATGTC	1340
QY	1343	GCTCTATGGAATGAAATGTTTGGAGGACCGAAATCTTGCATTTTGTAGTAC	1402
Db	1341	GCTCTATGGAATGAAATGTTTGGAGGACCGAAATCTTGCATTTTGTAGTAC	1399
QY	1403	TTTGAAGTAAATCAGACACCGGTGATTTTGTGTGTATATAAAGTACATTT	1462
Db	1400	TTTGAAGTAAATCAGACACCGGTGATTTTGTGTGTATATAAAGTACATTT	1459
QY	1463	GTCCTCGATTCGTGTAGTATGATCTTTCGATTTAGACGAAGTATCCTTGT	1522
Db	1460	GTCCTCGATTCGTGTAGTATGATCTTTCGATTTAGACGAAGTATCCTTGT	1519
QY	1523	ATTGAACAAAATATATCCACTTTGAAGACGGTCCCGTGTAGTATGATGAT	1582
Db	1520	ATTGAACAAAATATATCCACTTTGAAGACGGTCCCGTGTAGTATGATGAT	1579
QY	1583	CTTAAGCTGTCCAAAATTTTGGACGTGGCTGTTTAGATACAGTAGTCCCAT	1642
Db	1580	CTTAAGCTGTCCAAAATTTTGGACGTGGCTGTTTAGATACAGTAGTCCCAT	1639
QY	1643	ATTGATGAAAACAGTATATATCTTCAGGAACAGGGGATTCCTGTCTTCC	1702
Db	1640	ATTGATGAAAACAGTATATATCTTCAGGAACAGGGGATTCCTGTCTTCC	1699
QY	1703	TAGTCCCGAGATTTTTCCTCCAAATATCTTAAAAAGTACCTTCTGGTCA	1762
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QY	1763	AATTGATGTCTACAAATATGCTTTATAGCGTATCCTAGCTGATTCAGTTA	1822
Db	1760	AATTGATGTCTACAAATATGCTTTATAGCGTATCCTAGCTGATTCAGTTA	1819
QY	1823	TAAATACCCCTATAGTTTATGTACGAGAGAACTTATCCGATTTCTGAT	1882
Db	1820	TAAATACCCCTATAGTTTATGTACGAGAGAACTTATCCGATTTCTGAT	1879
QY	1883	TTATATGAAATGAAGCTGTAGCATAGACGATTAATCATTTGATTTT	1934
Db	1880	TTATATGAAATGAAGCTGTAGCATAGACGATTAATCATTTGATTTT	1931

[illegible]



Db 751 AACGAACTATTAGTTTTCATCATCAAAAAAAAAAAGATTCTCGTGGCGACAG 810  
Oy 812 CCAATCTCCATTTATGGGACACAGGCAACAAGAGTGGCTGCCAGAGAACCCAC 871  
Db 811 CCAATCTCCATTTATGGGACACAGGCAACAAGAGTGGCTGCCAGAGAACCCAC 870  
Oy 872 AAAAAACGATGATCTAACGAGGACAGC 899  
Db 871 AAAAAACGATGATCTAACGAGGACAGC 898

RESULT 13  
AX044095 898 bp DNA linear PAT 24-NOV-2000  
LOCUS Sequence 50 from Patent WO0066748.  
DEFINITION AX044095  
ACCESSION AX044095  
VERSION AX044095.1 GI:11342973  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sp.  
Oryza sp.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS Hawkes, T.R., Warner, S.A., Andrews, C.J., Bachoo, S. and  
Pickering, I.A.P.  
TITLE Herbicide resistant plants  
JOURNAL Patent: WO 0066748-A 50 09-NOV-2000;  
ZENECA LIMITED (GB)  
FEATURES  
source  
1. .898  
Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:52841"

## ORIGIN

Query Match 18.3%; Score 402; DB 6; Length 898;  
Best Local Similarity 99.3%; Pred. No. 8e-198;  
Matches 862; Conservative 0; Mismatches 2; Indels 4; Gaps 2;

Oy 33 CTAACTAACTATAGGAAAGCGTGTCTAAATATAAAGAGCCCTTATATATGTCGCC 92  
Db 34 CTAACTAACTATAGGAAAGCGTGTCTAAATATAAAGAGCCCTTATATATGTCGCC 93  
Oy 93 TGATACTAGAACTATAGGAAAGAACTCATCACTTATAGTGGCAATCGGCTTAA 152  
Db 94 TGATACTAGAACTATAGGAAAGAACTCATCACTTATAGTGGCAATCGGCTTAA 153  
Oy 153 TAAAAAAGAGTCGTACACTAGTTTGTCTTCTAGTAAATTAAGTGGAAAAATGAATC 212  
Db 154 TAAAAAAGAGTCGTACACTAGTTTGTCTTCTAGTAAATTAAGTGGAAAAATGAATC 213  
Oy 213 ATTATTTGCTTAAATATACGTTCACTCTCTGTCAATGAAGTTTATTCGAGGTAGCC 272  
Db 214 ATTATTTGCTTAAATATACGTTCACTCTCTGTCAATGAAGTTTATTCGAGGTAGCC 273  
Oy 272 ATTAATGTCATCAAACTCTTCTTGAATAAAAAATCTTCTAGCTGAATCAATGGGTAA 332  
Db 274 ATTAATGTCATCAAACTCTTCTTGAATAAAAAATCTTCTAGCTGAATCAATGGGTAA 333  
Oy 333 AGAGAGATATTTTAAAAAATAAGATGAATATCTGAACGTATCGGCAAG 392  
Db 334 AGAGAGATATTTTAAAAAATAAGATGAATATCTGAACGTATCGGCAAG 390  
Oy 393 ATTTAAACAT 452  
Db 391 ATTTAAACAT 450  
Oy 453 AGGACATGCTTACTACATCTCAATTTTATATATATATATATATATATATATATAT 512  
Db 451 AGGACATGCTTACTACATCTCAATTTTATATATATATATATATATATATATATAT 510

Oy 513 TATTATTTATCTTTTGGATTAGTGAAGTACTTACGACACACTTTGTCATGT 572  
Db 511 TATTATTTATCTTTTGGATTAGTGAAGTACTTACGACACACTTTGTCATGT 570  
Oy 573 GCATGTGAGTGACCTCTCCTC-ATPAGAAGTTCACTAGCGACACATCTCCATATGACT 631  
Db 571 GCATGTGAGTGACCTCTCCTCCTCAATACGTTCACTAGCGACACATCTCTATATGACT 630  
Oy 632 CGCCTATTTAAT 691  
Db 631 CGCCTATTTAAT 690  
Oy 692 CACTTTAAT 751  
Db 691 CACTTTAAT 750  
Oy 752 AACGAACCTATTAGTTTTCATATCAAAAAAAGAAATTTTGTCTGTGCGGACGC 811  
Db 751 AACGAACCTATTAGTTTTCATATCAAAAAAAGAAATTTTGTCTGTGCGGACGC 810  
Oy 812 CCAATCTCCATTTATGGGACACAGGCAACAAGAGTGGCTGCCACAGAACCCAC 871  
Db 811 CCAATCTCCATTTATGGGACACAGGCAACAAGAGTGGCTGCCACAGAACCCAC 870  
Oy 872 AAAAAACGATGATCTAACGAGGACAGC 899  
Db 871 AAAAAACGATGATCTAACGAGGACAGC 898

RESULT 14  
AX044183 898 bp DNA linear PAT 24-NOV-2000  
LOCUS Sequence 35 from Patent WO0066746.  
DEFINITION AX044183  
ACCESSION AX044183  
VERSION AX044183.1 GI:11343061  
KEYWORDS  
SOURCE  
Oryza sp.  
Oryza sp.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

## ORIGIN

Query Match 18.3%; Score 402; DB 6; Length 898;  
Best Local Similarity 99.3%; Pred. No. 8e-198;  
Matches 862; Conservative 0; Mismatches 2; Indels 4; Gaps 2;

Oy 33 CTAACTAACTATAGGAAAGCGTGTCTAAATATAAAGAGCCCTTATATATGTCGCC 92  
Db 34 CTAACTAACTATAGGAAAGCGTGTCTAAATATAAAGAGCCCTTATATATGTCGCC 93  
Oy 93 TGATACTAGAACTATAGGAAAGAACTCATCACTTATAGTGGCAATCGGCTTAA 152  
Db 94 TGATACTAGAACTATAGGAAAGAACTCATCACTTATAGTGGCAATCGGCTTAA 153  
Oy 153 TAAAAAAGAGTCGTACACTAGTTTGTCTTCTTCTAGTAAATTAAGTGGAAAAATGAATC 212  
Db 154 TAAAAAAGAGTCGTACACTAGTTTGTCTTCTTCTAGTAAATTAAGTGGAAAAATGAATC 213  
Oy 213 ATTATTTGCTTAAATATACGTTCACTCTCTGTCAATGAAGTTTATATATATATATAT 272  
Db 214 ATTATTTGCTTAAATATACGTTCACTCTCTGTCAATGAAGTTTATATATATATATAT 273



Oy		273	ATAATGTCATCAAACTCCTTGCTGAATPAAAAAACCCTTACGTAGCACTCAAGGGGTA	332	
Dd		274	ATAATGTCATCAAACTCTCTTGAAATPAAAAAATCTTTAGCTGAACCTCAATGGGTA	333	
Oy		333	AGAGAGATATTTTTTTTTTAAAAAAAATGAAATGAATATTTCTGAACGTATCGGCAAG	392	
Dd		334	AGAGAGATATTTTTTTTTT---AAAAAATATGAAATGAATATTTCTGAACGTATCGGCAAG	390	
Oy		393	ATTTPAACATATATATATATATTTTATATATGTTTGCAATTCGTTATATCGCACGTATTA	452	
Dd		391	ATTTPAACATATATATATATATATTTTATATATGTTTGCAATTCGTTATATCGCACGTATTA	450	
Oy		453	AGGACATGCTCACTCCCATCTCAATTTTATATAGTATPAAAGACAATGACTATATTTT	512	
Dd		451	AGGACATGCTCACTCCCATCTCAATTTTATATAGTATPAAAGACAATGACTATATTTT	510	
Oy		513	TATATATATCTTTTTTGCATTTAGATGCAAGGTACTTAACGACACACTTTGCTGCTAGT	572	
Dd		511	TATATATATCTTTTTTGCATTTAGATGCAAGGTACTTAACGACACACTTTGCTGCTAGT	570	
Oy		573	GCAATGTGAGTGCACCTCTCTC-ATACACGTTCAACTAGCCACACATCTCCATPATCACT	631	
Dd		571	GCATGTGAGTGCACCTCTCTCAATACAGTTCAACTAGCCACACATCTCTAATPATCACT	630	
Oy		632	CGCCATATTTAATACATTTTAGGTAGCAATCTGAATTAAGAAGCTTCAACATCACACAG	691	
Dd		631	CGCCATATTTAATACATTTTAGGTAGCAATCTGAATTAAGAAGCTTCAACATCACACAG	690	
Oy		692	CACCTTTTATATATCTAATAATACAAAAATATATTTTACAGATATGATGAAAAAGTATGA	751	
Dd		691	CACCTTTTATATATCTAATAATACAAAAATATATTTTACAGATATGATGAAAAAGTATGA	750	
Oy		752	AACGAACTATTTTAGTCTTTTTCACATACAAAAAAGAAATTTTGTCTGTCGCGGACG	811	
Dd		751	AACGAACTATTTTAGTCTTTTTCACATACAAAAAAGAAATTTTGTCTGTCGCGGACG	810	
Oy		812	CCAATCTCCCATAATTGGGCACACAGGCAACAAACAGATGCTGCCACAGAAACAACCCAG	871	
Dd		811	CCAATCTCCCATAATTGGGCACACAGGCAACAAACAGATGCTGCCACAGAAACAACCCAG	870	
Oy		872	AAAAAAAAAGATGATCTAACGGAGGACAGC	899	
Dd		871	AAAAAAAAAGATGATCTAACGGAGGACAGC	898	
RESULT 15					
AK120697					
LOCUS		752 bp	mRNA	linear	
DEFINITION			Oryza sativa (japonica cultivar-group) cDNA clone:J013170105, full insert sequence.		
ACCESSION		AK120697.1	GI:37990320		
VERSION		AK120697.1	GI:37990320		
KEYWORDS		FLI -cDNA; CAP trapper.			
SOURCE		Oryza sativa (japonica cultivar-group)			
ORGANISM		Oryza sativa (japonica cultivar-group)			
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
		Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;			
		Echinozoidae; Oryzeae; Oryza.			
REFERENCE		1	The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yarak,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Koike,K., Naito,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Onheuki,K., Shisshiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:: Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kuratsaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN, Kawai,J., Carrinci,P., Adachi,J., Atawa,K., Arakawa,T., Furuta,S.,		
AUTHORS					

[illegible]

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/clone="J013170105"

ORIGIN

Query Match 3.1%; Score 69; DB 15; Length 752;  
Best Local Similarity 100.0%; Pred.No. 7.1e-24;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1023 GGAGGATCCAAAGCAAGAGGAGGAGGACCGGACTAGAGAGAGCGGAG 1082  
|||  
Db 5 GGAGGATCCAAAGCAAGAGGAGGAGGACCGGACTAGAGAGCGGAG 64

QY 1083 CGACCGCCT 1091  
|||  
Db 65 CGACCGCCT 73

Search completed: April 21, 2006, 12:06:37  
Job time : 11142 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 21, 2006, 08:59:34 ; Search time 1221 Seconds  
(without alignments)  
11981.163 Million cell updates/sec

Title: US-10-541-315-1  
Perfect score: 2195  
Sequence: 1 aatccgaagaagttcttcgacac.....cacttcaccagcaagttc 2195

Scoring table: Gapop 60.0, Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size: 11  
Total number of hits satisfying chosen parameters: 9993364

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_21.\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001s:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003s:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004s:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2195	100.0	2195	13	AD01013 Regulator
2	1267	57.7	9361	3	Aa01285 Rice tran
3	1267	57.7	10639	3	Aa01286 Rice tran
4	1165	53.1	3032	13	AD792083
5	936	42.6	2191	14	ADY69039 GOS2 prim
6	402	18.3	898	3	AAC88400
7	402	18.3	898	3	AAC87195
8	73	3.3	719	10	ADK55377
9	73	3.3	724	10	ADK55377
10	73	3.3	725	10	ADK59227
11	73	3.3	782	10	ADK17562
12	73	3.3	808	12	ADJ39051 Plant CDN
13	29	1.3	48	3	AAC88379
14	29	1.3	48	3	AAC87162
15	27	1.2	12733	6	AB132090
16	24	1.1	24	10	ADJ36866
17	23	1.0	52	10	AD068856
18	23	1.0	8842	4	AAS45366
19	23	1.0	8842	6	ABK28203

C	20	22	1.0	22	10	AD06857	Adc06857 PCR prime
C	21	22	1.0	36	3	AAC88380	Aac88380 Primer GO
C	22	22	1.0	36	3	AAC87163	Aac87163 Rice GOS2
C	23	22	1.0	2000	11	AC138169	Ac138169 Rice secre
C	24	22	1.0	2195	13	AD01013	Ad01013 Regulator
C	25	22	1.0	6155	6	ABK28361	Abk28361 DNA trans
C	26	22	1.0	6233	6	ABN80127	Abn80127 Human chr
C	27	22	1.0	10105	6	ABL92285	Ab192285 Chemical1
C	28	22	1.0	11015	6	ABL49356	Ab149356 Human pol
C	29	22	1.0	11015	6	AD22336	Ad22336 Chemical1
C	30	22	1.0	12269	4	AAS46472	Aas46472 Tumour su
C	31	22	1.0	12269	6	ABJ33411	Abj33411 Human imm
C	32	22	1.0	107745	13	ABD33242	Abd33342 Human can
C	33	22	1.0	256493	11	ACN44514	Acn44514 Human gen
C	34	22	1.0	300000	12	AD86352	Ad86352 Human PTP
C	35	22	1.0	300001	12	AD014076	Ad014076 Human pro
C	36	21	1.0	345	13	ACN49828	Acn49828 Cotton pr
C	37	21	1.0	351	9	ACH31552	Ach31552 Human bon
C	38	21	1.0	360	2	AAV70862	Aav70862 Internal
C	39	21	1.0	415	14	AD270994	Ad270994 Human chr
C	40	21	1.0	460	8	ABZ73069	Abz73069 Rice leaf
C	41	21	1.0	479	5	ABV56511	Abv56511 Human pro
C	42	21	1.0	487	3	AA08525	Aa08525 Fusaarium
C	43	21	1.0	487	13	ADU52566	Adu52566 Fusaarium
C	44	21	1.0	487	14	AD290569	Ad290569 Fusaarium
C	45	21	1.0	598	6	AAS15016	Aas15016 Rice anth

ALIGNMENTS

RESULT 1	AD01013	standard; DNA; 2195 BP.
ID	AD01013	
AC	AD01013	
XX	21-OCT-2004	(first entry)
DT	Regulatory DNA sequence of the rice GOS2 gene SeqID 1.	
DE	regulatory; plant; rice; GOS2; non-monocotyledonous; transgenic; ds.	
KW	Oryza sativa.	
OS	WO2004065596-A2.	
XX	05-AUG-2004.	
XX	21-JAN-2004; 2004WO-EP000645.	
PF	21-JAN-2003; 2003EP-00075207.	
XX	(CROP-) CROPDSEIGN NV.	
XX	Hatzfeld Y, Inze D;	
PI	WPI; 2004-562175/54.	
XX	Use of a regulatory nucleic acid sequence for driving expression of an associated nucleic acid sequence in a non-monocotyledonous plant or plant cell.	
PT	Claim 1, SEQ ID NO 1; 25pp; English.	
PS	This invention relates to a novel isolated regulatory nucleic acid sequence that is useful in the field of plant molecular biology.	
XX	Specifically, it refers to a regulatory gene of the rice GOS2 gene that can drive expression of an associated nucleic acid sequence in a non-monocotyledonous plant or plant cell.	
CC	The present invention describes introducing a regulatory sequence that results in constitutive expression (with levels similar to that of CamV 35S) of an isolated or endogenous nucleic acid sequence in a transgenic non-monocotyledonous plant. In	

CC particular, a plant cell derived from either a fodder or forage legume,  
CC ornamental plant, food crop, tree or shrub, preferably from cotton,  
CC potato, tomato, cabbage, sugar beet, soybean, sunflower, or peas. This  
CC polynucleotide sequence is the regulatory sequence of the rice GOS2 gene  
CC of the invention.

XX  
SQ Sequence 2195 BP; 639 A; 426 C; 403 G; 727 T; 0 U; 0 Other;

Query Match 100.0%; Score 2195; DB 13; Length 2195;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATCGGAAAAGTTTCTGCAACCGTTTCACTCTCACTAACAATATAGGAAACGTGTGT 60  
DB 1 AATCGGAAAAGTTTCTGCAACCGTTTCACTCTCACTAACAATATAGGAAACGTGTGT 60  
QY 61 AATAATTAAGAGACCTTATATATAGTACGCTGAATATAGAACTATAGAAAACT 120  
DB 61 AATAATTAAGAGACCTTATATATAGTACGCTGAATATAGAACTATAGAAAACT 120  
QY 121 CATCCACCTACTTATAGTGGCAATCGGCTAAATTAATAAGAGTCCCTACACTAGTTTGT 180  
DB 121 CATCCACCTACTTATAGTGGCAATCGGCTAAATTAATAAGAGTCCCTACACTAGTTTGT 180  
QY 181 TTTCTTACTATTAATTAAGTGGGAAAATGAATCATTTTCTTGAATATATACCTTCAATC 240  
DB 181 TTTCTTACTATTAATTAAGTGGGAAAATGAATCATTTTCTTGAATATATACCTTCAATC 240  
QY 241 TCTGTCAAGAAATTAATTAATGAGGTATGAGCATATGTCATCAACCTCTTGAATA 300  
DB 241 TCTGTCAAGAAATTAATTAATGAGGTATGAGCATATGTCATCAACCTCTTGAATA 300  
QY 301 AAAAAATCTTTCTAGCTGAACTCAATGGGTAAAGAGAGATATTTTTTTAAAAAAAT 360  
DB 301 AAAAAATCTTTCTAGCTGAACTCAATGGGTAAAGAGAGATATTTTTTTAAAAAAAT 360  
QY 361 AGAATGAAGATATCTGAACTGATCGGCAAGAGTTTAAACATATATATATATATAT 420  
DB 361 AGAATGAAGATATCTGAACTGATCGGCAAGAGTTTAAACATATATATATATATAT 420  
QY 421 AGTTGTGATTCGTTATATGAGCATATTAAGGACATGCTTACTCATCTCAATTTT 480  
DB 421 AGTTGTGATTCGTTATATGAGCATATTAAGGACATGCTTACTCATCTCAATTTT 480  
QY 481 TATTTAGTATTAAGACAAATGACTTATTTTTATTTATCTTTTTTCAGTTAGATGC 540  
DB 481 TATTTAGTATTAAGACAAATGACTTATTTTTATTTATTTATTTTTCAGTTAGATGC 540  
QY 541 AAGGTACTTAGGACACACTTTGTGCTCATGTGATGTGTGAGTGCACCTCTCATAC 600  
DB 541 AAGGTACTTAGGACACACTTTGTGCTCATGTGATGTGTGAGTGCACCTCTCATAC 600  
QY 601 GTTCAACTTAGGACACACTTTGTGCTCATGTGATGTGTGAGTGCACCTCTCATAC 660  
DB 601 GTTCAACTTAGGACACACTTTGTGCTCATGTGATGTGTGAGTGCACCTCTCATAC 660  
QY 661 TCTGAATTCAGGACCTTCAACATCACTGACAGACCACTTTTAAATATCTAAAAATACA 720  
DB 661 TCTGAATTCAGGACCTTCAACATCACTGACAGACCACTTTTAAATATCTAAAAATACA 720  
QY 721 ATTAATTTTACAGAAATAGCATGAAAGATGAAGAGAACTATTTAGGTTTTTCAATACA 780  
DB 721 ATTAATTTTACAGAAATAGCATGAAAGATGAAGAGAACTATTTAGGTTTTTCAATACA 780  
QY 781 AAAAAAAGAAATTTTGTCTGCGGCGGAGCGGCAATCTCCCATATTTGGGACACAGGAA 840  
DB 781 AAAAAAAGAAATTTTGTCTGCGGCGGAGCGGCAATCTCCCATATTTGGGACACAGGAA 840  
QY 841 CAACAGAGTGGCTGCCACAGAACCAACCAAAAAAGATGATTTAAACGAGGACAGCA 900  
DB 841 CAACAGAGTGGCTGCCACAGAACCAACCAAAAAAGATGATTTAAACGAGGACAGCA 900  
QY 901 AGTCGCAACAACCTTTTAAACAGCAGGCTTTGCGGCAGAGAGAGAGAGGCAAG 960

DB 901 AGTCGCAACAACCTTTTAAACAGCAGGCTTTGCGGCAGAGAGAGAGAGGCAAG 960  
QY 961 AAAACCAAGCATCTCTCTCTCTCCCATCTAATAATTTCTCCCTTTTCCCTCTCTATA 1020  
DB 961 AAAACCAAGCATCTCTCTCTCTCCCATCTAATAATTTCTCCCTTTTCCCTCTCTATA 1020  
QY 1021 TAGAGAGCATCAAGCCAAAGAGAGAGACACCAAGAGACCGCATAGCAGAACCG 1080  
DB 1021 TAGAGAGCATCAAGCCAAAGAGAGAGACACCAAGAGACCGCATAGCAGAACCG 1080  
QY 1081 AGCAGCGCCTTCTTCAATCATATCTTCGCGTGAAGTTCTTGATCATCTTCCCTCC 1140  
DB 1081 AGCAGCGCCTTCTTCAATCATATCTTCGCGTGAAGTTCTTGATCATCTTCCCTCC 1140  
QY 1141 TCCACCTCTCTCTCAAGAGGATATGACCTTCGCTTGTCTTGAATTTATTTCTAGAT 1200  
DB 1141 TCCACCTCTCTCTCAAGAGGATATGACCTTCGCTTGTCTTGAATTTATTTCTAGAT 1200  
QY 1201 TGTGTAGTACGAGGCTTGTATAGAAAGGAGATCTGTATCTGTATGATTCCTGTCT 1260  
DB 1201 TGTGTAGTACGAGGCTTGTATAGAAAGGAGATCTGTATCTGTATGATTCCTGTCT 1260  
QY 1261 TGGATTTGGGATTAAGAGGGGCTTGTATGATTTGATAGTTATGATAGT 1320  
DB 1261 TGGATTTGGGATTAAGAGGGGCTTGTATGATTTGATAGTTATGATAGT 1320  
QY 1321 ATGGTTTTTCAATCGCTGAGAGCTATGGAATGAATAGTTTAAAGGATACGGAATCTT 1380  
DB 1321 ATGGTTTTTCAATCGCTGAGAGCTATGGAATGAATAGTTTAAAGGATACGGAATCTT 1380  
QY 1381 GCGATTTTGTGATACCTTTTGTGTGAGTAAATCAAGACACCGGTGATTTGTCTTGT 1440  
DB 1381 GCGATTTTGTGATACCTTTTGTGTGAGTAAATCAAGACACCGGTGATTTGTCTTGT 1440  
QY 1441 GTATTAAGATCAATTTTGTGTCTGATTTCTGATAGTCTTCTGATTTGACGA 1500  
DB 1441 GTATTAAGATCAATTTTGTGTCTGATTTCTGATAGTCTTCTGATTTGACGA 1500  
QY 1501 AGCTATCGCTTGTATTTATCCCTATTAAGAAATAATCAAACTTTGAAGCGGTCCCGT 1560  
DB 1501 AGCTATCGCTTGTATTTATCCCTATTAAGAAATAATCAAACTTTGAAGCGGTCCCGT 1560  
QY 1561 TGATGAGATTAAGATGATTTGATCTTAAAGCTGTCCAAATTTTGGCAGCTGGCTTTAG 1620  
DB 1561 TGATGAGATTAAGATGATTTGATCTTAAAGCTGTCCAAATTTTGGCAGCTGGCTTTAG 1620  
QY 1621 ATACAGTAGTCCCATACAGAAATTCATGAAGACAGTTATATCTCAGAGAACGAGGAT 1680  
DB 1621 ATACAGTAGTCCCATACAGAAATTCATGAAGACAGTTATATCTCAGAGAACGAGGAT 1680  
QY 1681 TCCCGTTCTTCGGAATTTGCTTAGTCCAGAAATTTTTTCCCAATATCTTAAAAAGT 1740  
DB 1681 TCCCGTTCTTCGGAATTTGCTTAGTCCAGAAATTTTTTCCCAATATCTTAAAAAGT 1740  
QY 1741 CACTTCTGCTTCAAGTCAATGAATGATTTGCTTCAAAATATGCTTTTATAGGTTATCC 1800  
DB 1741 CACTTCTGCTTCAAGTCAATGAATGATTTGCTTCAAAATATGCTTTTATAGGTTATCC 1800  
QY 1801 TAGCTGATGTTCACTTTATAGTATACCTTATAGTTTATGTTAGTGAAGAACTTATCC 1860  
DB 1801 TAGCTGATGTTCACTTTATAGTATACCTTATAGTTTATGTTAGTGAAGAACTTATCC 1860  
QY 1861 GATTTTCAATCTCATTTTAAATTAATTAAGAAAGAACTGATAGATAAGCATTAATTT 1920  
DB 1861 GATTTTCAATCTCATTTTAAATTAATTAAGAAAGAACTGATAGATAAGCATTAATTT 1920  
QY 1921 GGAATATTTTATTTATAGCTTTCAACCCCTTCAATTTCTGAGCTGAAAGTCTGGCATGA 1980  
DB 1921 GGAATATTTTATTTATAGCTTTCAACCCCTTCAATTTCTGAGCTGAAAGTCTGGCATGA 1980  
QY 1981 ACTGCTCAATTTTGTTTCAAAATTCATGATTAATCTATGATTAATCTCTTGTATC 2040

Db 1981 ACTGTCCTCAATTTGTTTCAAAATTCACATGCATTAATCAGATTAATCCTTGTATC 2040  
QY 2041 TACCTGTAGAAGTTTCTTTTGGTATATCTTGTACTGTGATAGAGAAAGAAATTAAT 2100  
Db 2041 TACCTGTAGAAGTTTCTTTTGGTATATCTTGTACTGTGATAGAGAAAGAAATTAAT 2100  
QY 2101 GAAGCTGTATCGGAGATAGTTATAGTCTGTTTCTTATGATTCATTTCTTTGTGCAATT 2160  
Db 2101 GAAGCTGTATCGGAGATAGTTATAGTCTGTTTCTTATGATTCATTTCTTTGTGCAATT 2160  
QY 2161 CTGTGTAGCTTTGCCATCTTCCACGACAAAGTTTC 2195  
Db 2161 CTGTGTAGCTTTGCCATCTTCCACGACAAAGTTTC 2195  
RESULT 2  
AAD01285/c  
ID AAD01285 standard; DNA; 9361 BP.  
XX AAD01285;  
XX  
XX 12-OCT-2000 (first entry)  
XX  
XX Rice transformation vector, pGOS2-hpt.  
XX  
XX Matrix Attachment Region; MAR; rice transformation vector; pGOS2-hpt;  
XX scaffold attachment region; gene expression; transgenic organism; ds.  
XX  
XX Synthetic.  
XX  
XX WO200032800-A1.  
XX  
XX 08-JUN-2000.  
XX  
XX 30-NOV-1999; 99WO-US028123.  
XX  
XX 01-DEC-1998; 98US-0110437P.  
XX  
XX (IDWC ) DOW AGROSCIENCES LLC.  
XX  
XX PA  
XX Van Der Geest AHM, Ainley WM, Cowen NM, Welter ME, Woosley AT;  
XX  
XX WPI; 2000-412345/35.  
XX  
XX An isolated DNA molecule for use as a matrix attachment region to  
XX increase expression of genes introduced in transformed plants comprises a  
XX PT 298 base pair sequence described in the specification.  
XX  
XX Example 3; Page 48-51; 73pp; English.  
XX  
XX The patent discloses a DNA molecule, useful as matrix attachment region  
XX (MAR) or scaffold attachment region, to increase the expression of genes  
XX introduced in transformed plants. MARs are located in non-transcribed  
XX regions of genes and form the physical boundaries of individual DNA  
XX loops. They are rich in adenosine and thymine bases and contain certain  
XX conserved sequence elements and structural features. They are about 300-  
XX 2000 bp in length. Increased levels of expression of DNA introduced into  
XX plants can be achieved by use of MAR. They can also reduce the position  
XX effect in transgenic organisms. The present DNA sequence is the rice  
XX transformation vector pGOS2-hpt, that contains a hygromycin selectable  
XX marker driven by the 35S promoter and a GOS2/GUS nos cassette (GOS2  
XX transcription initiation region/GUS structural gene/nos 3' untranslated  
XX region). The GOS2 transcription initiation region in this construct is  
XX comprised of 1010 bp of promoter and 170 bp of untranslated 5' leader  
XX interrupted by a 1100 bp intron sequence  
XX  
XX Sequence 9361 BP; 2449 A; 2285 C; 2190 G; 2435 T; 0 U; 2 Other;  
SQ  
Query Match 57.7%; Score 1267; DB 3; Length 9361;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1567; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 6472 AATATCACTCGCCTATTAAATCATTAGGTGCAATATCTGAATTCAGCACTCCACCA 6413  
QY 683 TCACGAGACCACTTTAAATTAATATCTAAATATCAAAAAATTAATTTTACAGATAGCATGA 742  
Db 6412 TCACGAGACCACTTTAAATTAATATCTAAATATCAAAAAATTAATTTTACAGATAGCATGA 6353  
QY 743 AAAGTATGAACGAACATAATTTAGTTTTCACATACAAAAAAGAAATTTTGTCTGCT 802  
Db 6352 AAAGTATGAACGAACATAATTTAGTTTTCACATACAAAAAAGAAATTTTGTCTGCT 6293  
QY 803 GCGCGAGCGCCAAATCTCCCATATTGGGCACACAGGCAACACAGTGGCTCCACAGAC 862  
Db 6292 GCGCGAGCGCCAAATCTCCCATATTGGGCACACAGGCAACACAGTGGCTCCACAGAC 6233  
QY 863 ACAACCCACAAAAAAGATGATCTAAGCGAGGACAGCAAGTCCGCAACCACTTTTAAACA 922  
Db 6232 ACAACCCACAAAAAAGATGATCTAAGCGAGGACAGCAAGTCCGCAACCACTTTTAAACA 6173  
QY 923 GCAGGCTTTGCGGCGAGGAGAGAGAGAGGACAAAGAAAAACAAGCATCTCTCTCTC 982  
Db 6172 GCAGGCTTTGCGGCGAGGAGAGAGAGAGGACAAAGAAAAACAAGCATCTCTCTCTC 6113  
QY 983 CCATCTAATAATTCCTCCCTCTTTTCCCTCTCTATATAGAGGCAATCCAGCAAGAA 1042  
Db 6112 CCATCTAATAATTCCTCCCTCTTTTCCCTCTCTATATAGAGGCAATCCAGCAAGAA 6053  
QY 1043 GAGGAGAGCAACCAAGGACAGCGCATAGCAGAACCGGACGCGCTCTTCATATCA 1102  
Db 6052 GAGGAGAGCAACCAAGGACAGCGCATAGCAGAACCGGACGCGCTCTTCATATCA 5993  
QY 1103 TATCTTCCGATCGAATCTTGTGTCATCTTCCCTCTCACTCTCTCTCTCAAGGATA 1162  
Db 5992 TATCTTCCGATCGAATCTTGTGTCATCTTCCCTCTCACTCTCTCTCTCAAGGATA 5933  
QY 1163 TGTGCTTCCGATCGAATCTTGTGTCATCTTGTGTCATCTTGTGTCATCTTGTGTCAT 1222  
Db 5932 TGTGCTTCCGATCGAATCTTGTGTCATCTTGTGTCATCTTGTGTCATCTTGTGTCAT 5873  
QY 1222 TAGGAAAGGGGATCTGTATCTGTATGATGATCTGATCTTGTGTAATAGGAGGTTTC 1282  
Db 5872 TAGGAAAGGGGATCTGTATCTGTATGATGATCTGATCTTGTGTAATAGGAGGTTTC 5813  
QY 1283 TTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1342  
Db 5812 TTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5753  
QY 1343 GCTCTATGGAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1402  
Db 5752 GCTCTATGGAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5693  
QY 1403 TTTGAGGTAAATGACAGACACCGGTGATTTTCTTGTGTATTAATAAGTATGTTGTTG 1462  
Db 5692 TTTGAGGTAAATGACAGACACCGGTGATTTTCTTGTGTATTAATAAGTATGTTGTTG 5633  
QY 1463 GTCCTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1522  
Db 5632 GTCCTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5573  
QY 1523 ATTGAACAAAAATTAATCAACTTTGAGAAGCGGTCCGTTGATGATGATGATGATGATGAT 1582  
Db 5572 ATTGAACAAAAATTAATCAACTTTGAGAAGCGGTCCGTTGATGATGATGATGATGATGAT 5513  
QY 1583 CTTAAGCCTGTGCAAAATTTTGGCAGCTGCTGTTTAATATACAGTATGCCATACGAA 1642  
Db 5512 CTTAAGCCTGTGCAAAATTTTGGCAGCTGCTGTTTAATATACAGTATGCCATACGAA 5453  
QY 1643 ATTGAACAAAAAGTATTAATCTCAGGAAACAGGGGATTCCTGTTCTTCCGATTTGCTT 1702  
Db 5452 ATTGAACAAAAAGTATTAATCTCAGGAAACAGGGGATTCCTGTTCTTCCGATTTGCTT 5393  
QY 1703 TAGTCCAGAAATTTTTCCTCAAAATATCTTAAAGTCACTTCTGTGTTCAAGTCAATG 1762

Db	5392	TAGTCCAGGAATTTTTTCCAAATACCTTAAAGACACTCTGGTCAAGTCAAG	5333
Oy	1763	AATTGATTGCTACAAATAATAGCTTTTATAGCTTATCCTAGCTGATGATTCAGTTATAG	1822
Db	5332	AATTGATTGCTACAAATAATAGCTTTTATAGCTTATCCTAGCTGATGATTCAGTTATAG	5273
Oy	1823	TAAATACCCCTATAGTTTATAGTCAGAGAAAGAACTTATCCGATTTTCATCTCATATTTTAA	1882
Db	5212	TAAATACCCCTATAGTTTATAGTCAGAGAAAGAACTTATCCGATTTTCATCTCATATTTTAA	5213
Oy	1883	TTATATGAAATGAACTGTAGCAATTAAGCAGTATTCATTTTGATTAATTTTTTATAGCTT	1942
Db	5212	TTATATGAAATGAACTGTAGCAATTAAGCAGTATTCATTTTGATTAATTTTTTATAGCTC	5153
Oy	1943	TCACCCCTCATATATCTGAGCTGAAAGTCGGCAGTAACTGCTCAATTTTGTTTCA	2002
Db	5152	TCACCCCTCATATATCTGAGCTGAAAGTCGGCAGTAACTGCTCAATTTTGTTTCA	5093
Oy	2003	AATTGACATCGATTATCTATCGATTATCCTCTTGATATCTACCTGTAGAAGTTCTTTTG	2062
Db	5092	AATTGACATCGATTATCTATCGATTATCCTCTTGATATCTACCTGTAGAAGTTCTTTTG	5033
Oy	2063	GTTATTTCTTGACCTGCTGATTATACGAAAGAAATTTATGAAGCTTATTCGGGATAGTTA	2122
Db	5032	GTTATTTCTTGACCTGCTGATTATACGAAAGAAATTTATGAAGCTTATTCGGGATAGTTA	4973
Oy	2123	TACTGCTGTCTTATGATTCAATTTCTTTGCGAGTTCTTGAGTACCTTGCCACTTTC	2182
Db	4972	TACTGCTGTCTTATGATTCAATTTCTTTGCGAGTTCTTGAGTACCTTGCCACTTTC	4913
Oy	2183	ACGAGCAAAAGTTC 2195	
Db	4912	ACGAGCAAAAGTTC 4900	

RESULT 3
AAD01286/C
ID AAD01286 standard; DNA; 10629 BP.
XX
XX
XX AC AAD01286;
XX
DT 12-OCT-2000 (first entry)
XX
DE Rice transformation vector, pARGOS2Af-hpt.
XX
DE Matrix Attachment Region; MAR; rice transformation vector; pARGOS2Af-hpt
XX
KW scaffold attachment region; gene expression; transgenic organism; ds.
RW
XX
OS Synthetic.
XX
Key Location/Qualifiers
FH misc_feature
FT 2735..3389
FT /*tag= a
FT /note= "Corresponds to nucleotides 14-668 of MAR dimer-2"
FT misc_feature
FT 7730..8384
FT /*tag= b
FT /note= "Corresponds to nucleotides 1-655 of MAR dimer-1"
XX
PN MO200032800-A1.
XX
PD 08-JUN-2000.
XX
PF 30-NOV-1999; 99MO-US028123.
XX
PR 01-DEC-1998; 98US-0110437P.
XX
PA (DOWC ) DOW AGROSCIENCES LLC.
XX
PI Van Der Geest AHM, Ainley WM, Cowen NM, Welter ME, Woosley AT;
XX
DR WPI; 2000-412345/35.
XX
An isolated DNA molecule for use as a matrix attachment region to

PT 298 increase expression of genes introduced in transformed plants comprises a base pair sequence described in the specification.

Example 3; Page 51-54; 73pp; English.

CC The patent discloses a DNA molecule, useful as matrix attachment region  
CC (MAR) or scaffold attachment region, to increase the expression of genes  
CC introduced in transformed plants. MARS are located in non-transcribed  
CC regions of genes and form the physical boundaries of individual DNA  
CC loops. They are rich in adenosine and thymine bases and contain certain  
CC conserved sequence elements and structural features. They are about 300-  
CC 2000 bp in length. Increased levels of expression of DNA introduced into  
CC plants can be achieved by use of MAR. They can also reduce the position  
CC effect in transgenic organisms. The present DNA sequence is the rice  
CC transformation vector pRCS2a-hpt, identical to the vector pGOS2-hpt,  
CC except that it contains a MAR dimer-2 positioned 5' to the GOS2  
CC transcription initiation region and the MAR dimer-1 positioned 3' to the  
CC nos 3' UTR (untranslated region). This vector is used to efficiently  
CC transform monocot plants like rice  
XX  
SQ Sequence 10629 BP; 2904 A; 2469 C; 2369 G; 2887 T; 0 U; 0 Other;

Query Match 57.7%; Score 1267; DB 3; Length 10629;

Best Local Similarity 99.6%; Pred.No. 0;  
Matches 1567; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	623	AAATATCACTGGCCCTATTTAAATACATTTTAGATGAGACAAATCTCGAATTCAGAGCACTTCACCA	682
Db	7111	AAATATCACTGGCCCTATTTAAATACATTTTAGATGAGACAAATCTCGAATTCAGAGCACTTCACCA	7053
QY	683	TCACCAGACCACTTTTATATATATATCTTAATAATACAAAAAATATTTTACAGATATGACATGA	742
Db	7051	TCACCAGACCACTTTTATATATATATCTTAATAATACAAAAAATATTTTACAGATATGACATGA	6992
QY	743	AAAGTATGAAACGAACATTTTAGGTTTTTCATACAAAAAATTTTGGCTCGT	802
Db	6991	AAAGTATGAAACGAACATTTTAGGTTTTTCATACAAAAAATTTTGGCTCGT	6932
QY	803	GCGCAGAGGCGCAATCTCCCATATTTGGGCACACAGGCAACAACAGATGGTCCACACAGA	862
Db	6931	GCGCAGAGGCGCAATCTCCCATATTTGGGCACACAGGCAACAACAGATGGTCCACACAGA	6872
QY	863	ACAAACCCACAAAAACGATGATCTACACGAGGACACGCAATGCCACACAACTTTTAA	922
Db	6871	ACAAACCCACAAAAACGATGATCTACACGAGGACACGCAATGCCACACAACTTTTAA	6812
QY	923	GCAGGCTTTGGGGCAGAGAGAGAGAGAGGAGGCAAAACCAAGCATCTCTCCTC	982
Db	6811	GCAGGCTTTGGGGCAGAGAGAGAGAGAGGAGGCAAAACCAAGCATCTCTCCTC	6755
QY	983	CCATCTATAAATTCCTCCCTTTTCCCTCTCTATATAGAGGCAATCCAAAGCCAGAA	1042
Db	6751	CCATCTATAAATTCCTCCCTTTTCCCTCTCTATATAGAGGCAATCCAAAGCCAGAA	6692
QY	1043	GAGGGAGAGCACAAAGGACACGCGCATCTGACGAAGCCGAGGACCGGCTTCTTCGATGCA	1102
Db	6691	GAGGGAGAGCACAAAGGACACGCGCATCTGACGAAGCCGAGGACCGGCTTCTTCGATGCA	6632
QY	1103	TATCTTCGCGATCGAATTCCTTGGATGATCTCTCCCTCCCTCCACCTCTCTCAAGGGTA	1162
Db	6631	TATCTTCGCGATCGAATTCCTTGGATGATCTCTCCCTCCCTCCACCTCTCTCAAGGGTA	6572
QY	1163	TGTGCCCCCTGGGTGTTCTTGGATTTATATGTTTACAGTTGTGTATACGGGCGTTGATGT	1222
Db	6571	TGTGCCCCCTGGGTGTTCTTGGATTTATATGTTTACAGTTGTGTATACGGGCGTTGATGT	6512
QY	1223	TAGGAAAAGGGGATCTGATCTGTGATGATTCCTGTTCTTGATTTGGGATAGAGGGGTTTC	1282
Db	6511	TAGGAAAAGGGGATCTGATCTGTGATGATTCCTGTTCTTGATTTGGGATAGAGGGGTTTC	6452
QY	1283	TTGATGTTGCATGTTATTCGGTTCCGTTTGATTTAGTATGATGTTTCAATGCTCTGAGGA	1342
Db	6451	TTGATGTTGCATGTTATTCGGTTCCGTTTGATTTAGTATGATGTTTCAATGCTCTGAGGA	6392

QY	1343	GCTCTATGGAAATGAATAGTGTTTAGGGATACGGAAATCTTGCGATTTTGTGATACCTTTG	1402
Db	6391	GCTCTATGGAAATGAATAGTGTTTAGGGATACGGAAATCTTGCGATTTTGTGATACCTTTG	6332
QY	1403	TTTGAAGTAAATCAGAGCACCGGATCTTGTGCTGGTATATAAAGTACATTTGTTTG	1462
Db	6331	TTTGAAGTAAATCAGAGCACCGGATCTTGTGCTGGTATATAAAGTACAGTTGTTTG	6272
QY	1463	GTCCTCGATTCGTAGTGATGCTTCTCGATTTTGAAGAAAGCTATCCTTTGTTTATCCCT	1522
Db	6271	GTCCTCGATTCGTAGTGATGCTTCTCGATTTTGAAGAAAGCTATCCTTTGTTTATCCCT	6212
QY	1533	ATTGGAACAAAATATATCCACTTTTGAACACGGTCCCCGTTGATGATGATGATGATTTGAT	1582
Db	6211	ATTGGAACAAAATATATCCACTTTTGAACACGGTCCCCGTTGATGATGATGATGATTTGAT	6152
QY	1583	CTTAAAGCTGTTCGCAAAATTTTGGACAGCTGGCTGTTTATGATACAGTAAAGCCCATCAGAA	1642
Db	6151	CTTAAAGCTGTTCGCAAAATTTTGGACAGCTGGCTGTTTATGATACAGTAAAGCCCATCAGAA	6092
QY	1643	ATTCATGAAAACAGTTATATCTTCAGGACAGGGGATTCCTGTCCTCCGATTTGCTT	1702
Db	6091	ATTCATGAAAACAGTTATATCTTCAGGACAGGGGATTCCTGTCCTCCGATTTGCTT	6032
QY	1703	TAGTCCCGCAATTTTTTTTCCCAAAATCTTAAAAAGCATTTCTGGTTCAGTTCAATG	1762
Db	6031	TAGTCCCGCAATTTTTTTTCCCAAAATCTTAAAAAGCATTTCTGGTTCAGTTCAATG	5972
QY	1763	AATTGATGTCTACAAATATATGCTTTTATAGCGTTATCCTAGCTGTAGTTCAGTTTATAGG	1822
Db	5971	AATTGATGTCTACAAATATATGCTTTTATAGCGTTATCCTAGCTGTAGTTCAGTTTATAGG	5912
QY	1823	TAAATACCCCTATAGTTTATGTCAGAGAAAGAACTTATCCGATTTCTGATCTCCATTTTAA	1882
Db	5911	TAAATACCCCTATAGTTTATGTCAGAGAAAGAACTTATCCGATTTCTGATCTCCATTTTAA	5852
QY	1883	TTATATGAAATGAAGCTGTGAGATGAAGCATATTCATTTGATTTATTTTATTTATAGCTT	1942
Db	5851	TTATATGAAATGAAGCTGTGAGATGAAGCATATTCATTTGATTTATTTTATTTATAGCTT	5792
QY	1943	TCACCCCTCATTTATTCCTGAGCTGAAGCTGTGAGTGAATGTCCTCAATTTTGTTCAT	2002
Db	5791	TCACCCCTCATTTATTCCTGAGCTGAAGCTGTGAGTGAATGTCCTCAATTTTGTTCAT	5732
QY	2003	AATTCAACATGATTATCTATGATTTATCTCTTGATCTACCTGTAGAAGTTTCTTTTG	2062
Db	5731	AATTCAACATGATTATCTATGATTTATCTCTTGATCTACCTGTAGAAGTTTCTTTTG	5672
QY	2063	GTTATTCCTTGACGCTGATTACAGAAAGAAATTTATGAAAGCTGTAATGGGATAGTTA	2122
Db	5671	GTTATTCCTTGACGCTGATTACAGAAAGAAATTTATGAAAGCTGTAATGGGATAGTTA	5612
QY	2123	TACTGCTGTGTTCTTATGATGATTTCTTTTGAGAGTCTTGAGTAGCTTGCCACATTC	2182
Db	5611	TACTGCTGTGTTCTTATGATGATTTCTTTTGAGAGTCTTGAGTAGCTTGCCACATTC	5552
QY	2183	ACGAGCAAAAGTTC 2195	
Db	5551	ACGAGCAAAAGTTC 5539	
RESULT 4			
ID	ADT92083	standard; DNA; 3032 BP.	
XX	ADT92083;		
XX	AC		
XX	DT	13-JAN-2005 (first entry)	
DE	PRO0129-CDS1585	expression cassette for MT2a.	
XX	MT2a;	plant growth; plant development; transgenic; genetic modification;	

KM	metallothionein; metal accumulation; abiotic stress; growth regulator;
KW	gene; ss.
XX	
XX	
OS	Synthetic.
XX	
XX	WO2004090142-A2.
PN	
XX	
PD	21-OCT-2004.
XX	
PF	14-APR-2004; 2004WO-EP050519.
XX	
PR	14-APR-2003; 2003EP-00076086.
XX	
PA	(CROP-) CROPDESIGN NV.
XX	
PI	Sanz Molinero AI;
XX	
DR	WPI; 2004-748770/73.
XX	
PT	Modifying plant growth and development for altering growth
PT	characteristics in plants, comprises introducing a genetic modification
PT	in the plant and selecting, modulated expression of a nucleic acid
PT	encoding a metallothionein protein.

Claim 13; SEQ ID NO 7; 49pp; English.

WPI; 2004-748770/73.

Sanz Molinero AI;

(CROP-) CROPDESIGN NV.

14-APR-2003; 2003EP-00076086.

14-APR-2004; 2004WO-EP050519.

21-OCT-2004.

WO2004090142-A2.

**Synthetic.**

gene; 88.

**jo.rng**



Qy 803 GCGGAGCGCCATCTCCCATATTTGGGACACAGGCAACAAGAGTGCGTCCACAGA 862  
Db 801 GGGCAGCGCCATCTCCCATATTTGGGACACAGGCAACAAGAGTGCGTCCACAGA 860  
Qy 863 ACAACCCACAAAACGATGATCTAACGGAGACAGCAAGTCCGGACAACCTTTTAA 922  
Db 861 ACAACCCACAAAACGATGATCTAACGGAGACAGCAAGTCCGGACAACCTTTTAA 920  
Qy 923 GCAAGCTTTGGCGCAGAGAGAGAGAGCAAAAGAAAACAAGCATCTCTCTCTC 982  
Db 921 GCAAGCTTTGGCGCAGAGAGAGAGAGCAAAAGAAAACAAGCATCTCTCTCTC 980  
Qy 983 CCATCTATAAATCT 1042  
Db 981 CCATCTATAAATCT 1040  
Qy 1043 GAGGAGAGACCAAGGAGACAGGAGACAGGAGAGAGAGAGAGAGAGAGAGAGAG 1102  
Db 1041 GAGGAGAGACCAAGGAGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1100  
Qy 1103 TATCTTCCGGTGAAGTCTTGGTGCATCTCTCCCTCTCTCTCTCTCTCTCTCT 1162  
Db 1101 TATCTTCCGGTGAAGTCTTGGTGCATCTCTCCCTCTCTCTCTCTCTCTCTCT 1160  
Qy 1163 TGTGCTTCTCGGTGTTCTTGGATTTATTTGTTAGTGTGTAGTACGGGCGTTGAT 1222  
Db 1161 TGTGCTTCTCGGTGTTCTTGGATTTATTTGTTAGTGTGTAGTACGGGCGTTGAT 1220  
Qy 1223 TAGGAAAGGGGATCTGTATCTGTAGTATCTGTCTTGGATTTGGGATAGAGGGTTC 1282  
Db 1221 TAGGAAAGGGGATCTGTATCTGTAGTATCTGTCTTGGATTTGGGATAGAGGGTTC 1280  
Qy 1283 TTGATGTTGCATGTTATCGGTTCCGTTTGATTTAGTATGTTGTTTCAATCGTCTGAGA 1342  
Db 1281 TTGATGTTGCATGTTATCGGTTCCGTTTGATTTAGTATGTTGTTTCAATCGTCTGAGA 1340  
Qy 1343 GCTTATGAGAAATGAATGTTTAAAGGTAAGGATCTTCCGATTTTGTGATGATCTTTTG 1402  
Db 1341 GCTTATGAGAAATGAATGTTTAAAGGTAAGGATCTTCCGATTTTGTGATGATCTTTTG 1400  
Qy 1403 TTTGAGGTAATATCAGAGACCGGTGATTTTGTGATGTAATTAAGATGATTTGTTTG 1462  
Db 1401 TTTGAGGTAATATCAGAGACCGGTGATTTTGTGATGTAATTAAGATGATTTGTTTG 1460  
Qy 1463 GTCTCGATTTCTGATGATGATCTTCTCGATTTGACGAATCTTCTTGTATTTCCCT 1522  
Db 1461 GTCTCGATTTCTGATGATGATCTTCTCGATTTGACGAATCTTCTTGTATTTCCCT 1520  
Qy 1523 ATTTGAACAAAATTAATCCAACTTTGAAACGGTCCCGTTGATGATGATGATTTGAT 1582  
Db 1521 ATTTGAACAAAATTAATCCAACTTTGAAACGGTCCCGTTGATGATGATGATTTGAT 1580  
Qy 1583 CTTAAGCCCTGTCGCAAAATTTGCAAGTGGCTTTTGTAGTATAGATGCCCATACGAA 1642  
Db 1581 CTTAAGCCCTGTCGCAAAATTTGCAAGTGGCTTTTGTAGTATAGATGCCCATACGAA 1640  
Qy 1643 ATTTGATGAAAACAGTTATATCTCAGAACAGGGGATCCCTGTTCTTCCGATTTGCTT 1702  
Db 1641 ATTTGATGAAAACAGTTATATCTCAGAACAGGGGATCCCTGTTCTTCCGATTTGCTT 1700  
Qy 1703 TAGTCCGAGAAATTTTTCCTCAAAATATCTTAAAGATCACTTTCGATTTCAATG 1762  
Db 1701 TAGTCCGAGAAATTTTTCCTCAAAATATCTTAAAGATCACTTTCGATTTCAATG 1760  
Qy 1763 AATTGATTTGCTACAAATATGCTTTTATAGCGTTATCCGATGATGATTTATAGG 1822  
Db 1761 AATTGATTTGCTACAAATATGCTTTTATAGCGTTATCCGATGATGATTTATAGG 1820  
Qy 1823 TAAATCCCTATAGTTTATGTCAGAGAAACTTATCCGATTTGATCTCCATTTTAA 1882  
Db 1821 TAAATCCCTATAGTTTATGTCAGAGAAACTTATCCGATTTGATCTCCATTTTAA 1880  
Qy 1883 TTATATGAATGAACGTAGCATTAAGCATTAATTTGATTTATTTTATTTAGCTT 1942

Db 1881 TTATATGAATGAACGTAGCATTAAGCATTAATTTGATTTATTTTATTTAGCTC 1940  
Qy 1943 TCACCCCTTCAATTAATTTGAGCTGAAAGTCTGAGATGAACTGTCTCAATTTGTTTCA 2002  
Db 1941 TCACCCCTTCAATTAATTTGAGCTGAAAGTCTGAGATGAACTGTCTCAATTTGTTTCA 2000  
Qy 2003 AATTCAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2062  
Db 2001 AATTCAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2060  
Qy 2063 GTTATTCCTTGAACGCTTGAATTAACAGAAATTTTATGAGTGTATGGGATGATTA 2122  
Db 2061 GTTATTCCTTGAACGCTTGAATTAACAGAAATTTTATGAGTGTATGGGATGATTA 2120  
Qy 2123 TACTGCTGTTCTTATGATTAATTTCTTGTGAGAGTCTTGTGATCTTCCACTTTC 2182  
Db 2121 TACTGCTGTTCTTATGATTAATTTCTTGTGAGAGTCTTGTGATCTTCCACTTTC 2180  
Qy 2183 ACCAGCAAAAGTTC 2195  
Db 2181 ACCAGCAAAAGTTC 2193

RESULT 5  
ADY69039  
ID ADY69039 standard; DNA; 2191 BP.  
XX  
AC ADY69039;  
XX  
DT 02-JUN-2005 (first entry)  
XX  
DE GOS2 promoter DNA.  
XX  
KW plant; crop improvement; B-type cyclin dependent kinase; CDK; ds;  
KW promoter; GOS2.  
XX  
OS unidentified.  
XX  
PN WO2005024029-A2.  
XX  
PD 17-MAR-2005.  
XX  
PF 03-SEP-2004; 2004WO-EP052035.  
XX  
PR 05-SEP-2003; 2003EP-00077811.  
XX  
PA (CROP-) CROPDESIGN NV.  
XX  
PI Broekaert W, Frankard V, Hatzfeld Y, Mironov V;  
XX  
DR WPI, 2005-223384/23.  
XX  
PT Improving plant growth characteristics, e.g. increased yield, increased  
PT growth rate, or modified architecture, comprises increasing expression,  
PT activity and/or levels in a plant of B-type cyclin dependent kinase.  
XX  
PS Disclosure; SEQ ID NO 15; 79bp; English.  
XX  
CC Improving plant growth characteristics, e.g. increased yield, increased  
CC growth rate, or modified architecture, comprises increasing expression in  
CC a plant of a nucleic acid encoding a B-type cyclin dependent kinase (CDK)  
CC protein and/or increasing activity and/or levels in a plant of a B-type  
CC CDK protein. INDEPENDENT CLAIMS are also included for: plants obtained  
CC using the method above; construct comprising (i) a B-type CDK  
CC gene/nucleic acid encoding a B-type CDK protein, or (ii) a nucleic acid  
CC encoding a CDK mutant, which CDK mutant comprises at least one of the 7  
CC amino acid position changes or at least one of the 8 amino acid position  
CC changes listed in the disclosure, (iii) one or more control sequences  
CC capable of driving expression of the nucleic acid of (i) or (ii), and  
CC optionally (iv) a transcription termination sequence; a method for  
CC producing transgenic plant having improved growth characteristics, e.g.  
CC increased yield, increased growth rate, or modified architecture, which

growth characteristics are improved relative to growth characteristics of corresponding wild type plants; transgenic plant having improved growth characteristics, e.g. increased yield, increased growth rate, or modified architecture, the plant has increased expression of a B-type CDK nucleic acid and/or increased activity and/or levels in a plant of a B-type CDK protein relative to corresponding wild type plants; a composition comprising a protein comprising a sequence of 309, 311, or 315 amino acids (EVEN SEQ ID NOS: 2-6), or its homologue, derivative, or active fragment, used as a growth regulator; a screening method for identifying mutant plant CDKs having enhanced CDK activity relative to corresponding non-mutated plant CDKs; a screening method for identifying substantially non-active plant CDKs, but are capable of binding to plant ICKs; mutant CDKs obtained using the methods of (6) and (7), where the mutants bind to cyclin but not to ICK as listed in the disclosure, or where the mutants bind to ICK but not to cyclin as listed in the disclosure; an isolated nucleic acid molecule comprising (i) a nucleic acid encoding a CDK mutant comprising any of the 5 sequences of 294 amino acids each (SEQ ID NOS: 9-13), or (ii) a nucleic acid molecule encoding a homologue, derivative or active fragment of a CDK mutant of SEQ ID NOS: 9-11, where the homologue, derivative or active fragment comprised at least one of the 7 amino acid position changes or at least one of the 8 amino acid position changes listed in the disclosure; (iii) a nucleic acid capable of hybridizing with a nucleic acid of (i) or (ii), where the hybridizing sequence encodes an amino acid comprising at least one of the 7 amino acid position changes or at least one of the 8 amino acid position changes listed in the disclosure; (iv) a nucleic acid of (i) which is degenerate as a result of the genetic code; (v) allelic variants of (i) to (iv), where the allelic variant encodes an amino acid comprising at least one of the 7 amino acid position changes or at least one of the 8 amino acid position changes listed in the disclosure, or (vi) alternative splice variants of nucleic acid of (i) to (v), where the alternative splice variants encodes an amino acid comprising at least one of the 7 amino acid position changes or at least one of the 8 amino acid position changes listed in the disclosure; and a CDK mutant comprising (i) an amino acid sequence of SEQ ID NOS: 9-13, or (ii) a fragment of SEQ ID NOS: 9-13 where the fragment comprises at least one of the 7 amino acid position changes or at least one of the 8 amino acid position changes listed in the disclosure. Preferred Method: Increasing expression is effected by introducing and expressing in a plant a B-type CDK nucleic acid. The B-type CDK is derived from a plant, algal, or fungal source. The B-type CDK derived from a plant is from a dicotyledonous plant, preferably from the family Brassicaceae, specifically Arabidopsis thaliana. The B-type CDK is a class 1 B-type CDK, preferably a CDK B1,1 or CDK B1,2 from A. thaliana. The B-type CDK is a class 2 B-type CDK, preferably a CDK B2,2 from A. thaliana. The CDK B1,1 nucleic acid comprises a sequence of 930 bp (SEQ ID NO: 1), or its portion, or a nucleic acid capable of hybridizing to SEQ ID NO: 1, and where the CDK B1,1 protein comprises a sequence of SEQ ID NO: 2 or its homologue, derivative or active fragment. The CDK B1,2 nucleic acid comprises a sequence of 936 bp (SEQ ID NO: 3), or its portion, or a nucleic acid capable of hybridizing to SEQ ID NO: 3, and where the CDK B1,2 protein comprises a sequence of SEQ ID NO: 4 or its homologue, derivative or active fragment. The CDK B2,2 nucleic acid comprises a sequence of 948 bp (SEQ ID NO: 5), or its portion, or a nucleic acid capable of hybridizing to SEQ ID NO: 5, and where the CDK B2,2 protein comprises a sequence of SEQ ID NO: 6 or its homologue, derivative or active fragment. The B-type CDK is a variant nucleic acid or variant amino acid, e.g. functional portions of, sequences capable of hybridizing to, alternative splice variants of, or allelic variants of a B-type CDK nucleic acid/gene, homologues, derivatives, or active fragments of a B-type CDK protein, or mutant B-type CDKs. The expression of the CDK B1,1 nucleic acid is driven by a promoter active in young, expanding tissue, preferably where the promoter is beta expansin promoter. The expression of CDK B1,2 nucleic acid/CDK B2,2 nucleic acid is driven by a constitutive promoter, specifically a GOS 2 promoter. The increased yield comprises increase in area, increase in the number of panicles, increase in height, increase in the number of seeds, increase in the number of filled seed, increase in total weight of seeds, increase in thousand kernel weight (TKW), or an increase in harvest index, each relative to control plants. The modified architecture includes increase in aboveground area, increase in the number of panicles or increase in height. Producing transgenic plant having improved growth characteristics, e.g. increased yield, increased growth rate, or modified architecture, which growth characteristics are

improved relative to growth characteristics of corresponding wild type plants, comprises introducing into a plant or a plant cell a B-type CDK gene/nucleic, or a nucleic acid encoding a CDK mutant comprising at least one of the 7 amino acid position changes listed in the disclosure, and cultivating the plant cell under conditions promoting regeneration and mature plant growth. Identifying mutant plant CDKs having enhanced CDK activity relative to corresponding non-mutated plant CDKs comprises providing plant-derived CDK mutants, identifying cyclin dependent kinase inhibitor (ICK) non reacting mutants, identifying mutants having cyclin-binding activity, and optionally a yeast complementation assay on resultant mutants, identifying substantially non-active plant CDKs, but are capable of binding to plant ICKs, comprises providing plant-derived CDK mutants, identifying plant-derived ICK binding mutants, and identifying non-cyclin binding mutants. The CDK mutants are provided by providing a wild type plant CDK and mutating the CDK at least 1 amino acid position. Preferred Transgenic Plant: The plant is a monocotyledonous plant. The CDK B-type nucleic or CDK B-type amino acid is useful for improving the growth characteristics of a plant, the growth characteristics is increased yield, increased growth rate, or modified architecture (claimed).

XX Sequence 2191 BP; 638 A; 431 C; 403 G; 719 T; 0 U; 0 Other;

Query Match 42.6%; Score 936; DB 14; Length 2191;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1306; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY	623	AAATACACGCGCTTAAATACATTTAGTGAATATCTGAATCAAGCACTTCACCA	682
DB	621	AAATACACGCGCTTAAATACATTTAGTGAATATCTGAATCAAGCACTTCACCA	680
QY	683	TCACGACGACCTTTTAAATATATATCAAAATAATTTTACAGAAATAGCATGA	742
DB	681	TCACGACGACCTTTTAAATATATATCAAAATAATTTTACAGAAATAGCATGA	740
QY	743	AAAGTATGAACGAACTATTAGTTTTCATATACAAAATAAAGAAATTTGCTCGT	802
DB	741	AAAGTATGAACGAACTATTAGTTTTCATATACAAAATAAAGAAATTTGCTCGT	800
QY	803	GGCGGACGCGCATCTCCCATATTTGGGACACAGGCAACAGAGATGGCTGCCACGA	862
DB	801	GGCGGACGCGCATCTCCCATATTTGGGACACAGGCAACAGAGATGGCTGCCACGA	860
QY	863	ACAACCAACAATAAAGATATCTAAGAGACAGCAAGTCGCAACAACCTTTTACA	922
DB	861	ACAACCAACAATAAAGATATCTAAGAGACAGCAAGTCGCAACAACCTTTTACA	920
QY	923	GGAGGCTTTGCGCCAGAGAGAGAGAGAGGCAAAAGAAACCAAGCATCTCTCTC	982
DB	921	GGAGGCTTTGCGCCAGAGAGAGAGAGAGGCAAAAGAAACCAAGCATCTCTCTC	980
QY	983	CAATCTATTAATTTCTCTCCCTTTTCCCTCTCTATATAGAGGATCCAGCAAGAA	1042
DB	981	CAATCTATTAATTTCTCTCCCTTTTCCCTCTCTATATAGAGGATCCAGCAAGAA	1040
QY	1043	GAGGAGAGACCAAGAGACACCGACTAGCAGAACCGAGCGCCTTTCTCATCA	1102
DB	1041	GAGGAGAGACCAAGAGACACCGACTAGCAGAACCGAGCGCCTTTCTCATCA	1100
QY	1103	TATCTTCGCGTGAAGTTTGTGATCTCTTCTCTCACTCTCTCTCAAGGGA	1162
DB	1101	TATCTTCGCGTGAAGTTTGTGATCTCTTCTCTCACTCTCTCTCAAGGGA	1160
QY	1163	TGTGCTTCGCTGTGTTCTTGATTTATTTGTTCTAGTGTGTATGACGGGGTGAAT	1222
DB	1161	TGTGCTTCGCTGTGTTCTTGATTTATTTGTTCTAGTGTGTATGACGGGGTGAAT	1220
QY	1223	TAGGAAGGGAATCTGATCTGATGATCTCTGTTCTTGATTTGGATAGAGGGTTC	1282
DB	1221	TAGGAAGGGAATCTGATCTGATGATCTCTGTTCTTGATTTGGATAGAGGGTTC	1280
QY	1283	TTGATTTGATGATTTATCGGTTTGGTTGATTTAGTATGATGATTTTCAATCTCTGAGA	1342

Db 1281 TTGATGTCAGATGATTCGGTTCGGTTGATTAAGTATGCTTTCAATCGTCGAGAA 1340  
Qy 1343 GCTATATGAAATGAATGTTTAGGGTACGGAATCTTCGATTTGTGATGACCTTTTG 1402  
Db 1341 GCTATATGAAATGAATGTTTAGGGTACGGAATCTTCGATTTGTGATGACCTTTTG 1399  
Qy 1403 TTTGAGGTAAATTCAGAGACCGGTGATTTTGGTGTAAATAAAAGTACATTTGTTTG 1462  
Db 1400 TTTGAGGTAAATTCAGAGACCGGTGATTTTGGTGTAAATAAAAGTACATTTGTTTG 1459  
Qy 1463 GTCCTGATTCGTGATGATGCTTCGATTTGAGAAAGTATCCTTTGTTTATCCCT 1522  
Db 1460 GTCCTGATTCGTGATGATGCTTCGATTTGAGAAAGTATCCTTTGTTTATCCCT 1519  
Qy 1523 ATTTGAACAAAATTAATCAACTTTTGAAAGACGGTCCGCTGATGATGAATGATGAT 1582  
Db 1520 ATTTGAACAAAATTAATCAACTTTTGAAAGACGGTCCGCTGATGATGAATGATGAT 1579  
Qy 1583 CTTTAAAGCTGTCCAAAATTTCCGAGCTGCTGTTTAAATACAGTATGTCCTCAACGA 1642  
Db 1580 CTTTAAAGCTGTCCAAAATTTCCGAGCTGCTGTTTAAATACAGTATGTCCTCAACGA 1639  
Qy 1643 ATTCATGAAACAGTATATATCTCAGAAACAGGGGATTCCTGTTCTTCGATTTGCTT 1702  
Db 1640 ATTCATGAAACAGTATATATCTCAGAAACAGGGGATTCCTGTTCTTCGATTTGCTT 1699  
Qy 1703 TAGTCCAGAAATTTTTCCTCAAAATCTTAAAGTACATTTCTGTTCACTTCAATG 1762  
Db 1700 TAGTCCAGAAATTTTTCCTCAAAATCTTAAAGTACATTTCTGTTCACTTCAATG 1759  
Qy 1763 AATTGATTCCTCAAAATTAATGCTTTTAAAGCTTATACGCTGATGATGATGATGAT 1822  
Db 1760 AATTGATTCCTCAAAATTAATGCTTTTAAAGCTTATACGCTGATGATGATGATGAT 1819  
Qy 1823 TAATACCCCTATAGTTTACTCAGAGAAAGTATCCGATTTGATTCGATTTTAA 1882  
Db 1820 TAATACCCCTATAGTTTACTCAGAGAAAGTATCCGATTTGATTCGATTTTAA 1879  
Qy 1883 TTATATGAATGAACGTATGATTAAGCAATATTCATTTGATTTATTTT 1934  
Db 1880 TTATATGAATGAACGTATGATTAAGCAATATTCATTTGATTTATTTT 1931

RESULT 6  
AAC88400  
ID AAC88400 standard; DNA; 898 BP.  
XX  
AC AAC88400;  
XX  
DT 02-MAR-2001 (first entry)  
XX  
DE Rice GOS2 enhancer.  
XX  
KM Glyphosate, 5-enolpyruvylshikimate phosphate synthase, EPSPS;  
XX herbicide resistance; ss.  
XX  
OS Oryza sativa.  
XX  
PN MO200066746-A1.  
XX  
PD 09-NOV-2000.  
PF 20-APR-2000; 2000WO-GB001559.  
XX  
PR 29-APR-1999; 99GB-000099971.  
PR 29-APR-1999; 99GB-000099972.  
PR 29-JUL-1999; 99GB-00017837.  
PR 29-JUL-1999; 99GB-00017842.  
PR 21-DEC-1999; 99GB-00030190.  
PR 21-DEC-1999; 99GB-00030206.  
PR 21-DEC-1999; 99GB-00030214.  
PR 21-DEC-1999; 99GB-00030216.  
XX

PA (ZENE ) ZENECA LTD.  
XX  
PI Hawkes TR, Warner SAJ, Andrews CJ, Bachoo S, Pickerill AP;  
XX  
DR WPI; 2000-679763/66.  
XX  
PT Novel polynucleotide encoding the rice 5-enolpyruvylshikimate phosphate  
XX  
PT synthase, used to produce glyphosate tolerant or resistant plants.  
XX  
PS Disclosure; Page 55; 85pp; English.  
XX  
CC The present invention relates to a glyphosate resistant rice 5-  
CC enolpyruvylshikimate phosphate synthase (EPSPS) gene. This gene can be  
CC used to produce plant tissue and/or morphologically normal fertile whole  
CC plants which are tolerant or resistant to glyphosate herbicide, and in  
CC the production of a herbicidal target for the high throughput in vitro  
CC screening of potential herbicides  
XX  
SQ Sequence 898 BP; 320 A; 166 C; 137 G; 275 T; 0 U; 0 Other;  
Query Match 18.3%; Score 402; DB 3; Length 898;  
Best Local Similarity 99.3%; Pred. No. 2.1e-176;  
Matches 862; Conservative 0; Mismatches 2; Indels 4; Gaps 2;  
Qy 33 CTAATTAACATATATGGAACGTGTGCTAAATATATTAATGAGACTTATATATGAGGC 92  
Db 34 CTAATTAACATATATGGAACGTGTGCTAAATATATTAATGAGACTTATATATGAGGC 93  
Qy 93 TGATACACAGAACTATATGAGAAACATCATCACTTCTTAAAGGCAATCGGGCTAAA 152  
Db 94 TGATACACAGAACTATATGAGAAACATCATCACTTCTTAAAGGCAATCGGGCTAAA 153  
Qy 153 TAAAAAGAGTCGCTACACTAGTTTCTTTTCTTAAATTAAGTGGAAATGAATC 212  
Db 154 TAAAAAGAGTCGCTACACTAGTTTCTTTTCTTAAATTAAGTGGAAATGAATC 213  
Qy 213 ATATATGCTTGAATATATGCTTACATCTCTGTCAATGAAGTAAATATTTGAGATGCC 272  
Db 214 ATATATGCTTGAATATATGCTTACATCTCTGTCAATGAAGTAAATATTTGAGATGCC 273  
Qy 273 ATATATGCTTGAATATATGCTTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 332  
Db 274 ATATATGCTTGAATATATGCTTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 333  
Qy 333 AGAGAGATATTTTAAAAAATGAATGAATGATATTCGAGATTCGCAAG 392  
Db 334 AGAGAGATATTTTAAAAAATGAATGAATGATATTCGAGATTCGCAAG 390  
Qy 393 ATTTAAGATATATATATATATATTTTATGTTTGTGCACTTGTATATCGACGTATTA 452  
Db 391 ATTTAAGATATATATATATATATTTTATGTTTGTGCACTTGTATATCGACGTATTA 450  
Qy 453 AGGACATGCTTACCTCACTCAATTTTATTTAGTATTAAGCAATGACTTATTT 512  
Db 451 AGGACATGCTTACCTCACTCAATTTTATTTAGTATTAAGCAATGACTTATTT 510  
Qy 513 TATTTATATCTTTTTCGATTAATGATGCAAGTACTTAAGCACAACCTTTGTGCTAGT 572  
Db 511 TATTTATATCTTTTTCGATTAATGATGCAAGTACTTAAGCACAACCTTTGTGCTAGT 570  
Qy 573 GCATGTGTAGTGCACCTCTCAATATACGTTCAACAGCACACATCTCTAAATATCACT 631  
Db 571 GCATGTGTAGTGCACCTCTCAATATACGTTCAACAGCACACATCTCTAAATATCACT 630  
Qy 632 GGCCTATTTATATATGATTAAGTATGATCAATCAAGCATCACTCACTCAAGAC 691  
Db 631 GGCCTATTTATATATGATTAAGTATGATCAATCAAGCATCACTCACTCAAGAC 690  
Qy 692 CACTTTTATATATATCAAAAAATATATTTTATCAGATATGATGATGATGATGATGATGAT 751  
Db 691 CACTTTTATATATATCAAAAAATATATTTTATCAGATATGATGATGATGATGATGATGAT 750  
Qy 752 AACGAATATTTAGGTTTTCACATACAAAAAAGAAATTTTGTCTGTGCGGAGCG 811

Db	751	AACGACATCTTTAGGTTTTCACATACAAAAAAGAAATTTTGTCTGTGGCGAGCG	810
Qy	812	CCAAATCTCCCATATTTGGGACACAGGCCAACACAGAGTGGCTGCCACAGAACCAACCCAC	871
Db	811	CCAAATCTCCCATATTTGGGACACAGGCCAACACAGAGTGGCTGCCACAGAACCAACCCAC	870
Qy	872	AAAAAACGATGATCTTACCGAGGACGACG	899
Db	871	AAAAAACGATGATCTTACCGAGGACGACG	898
RESULT 7			
ID	AAC87195	standard; DNA; 898 BP.	
AC	AAC87195;		
XX			
DT	09-MAR-2001	(first entry)	
DE	Rice	GOS2 promoter enhancer element, SEQ ID NO:50.	
XX			
KW	Rice BPSPS; 5-enolpyruvylshikimate phosphate synthase;		
KM	glyphosate resistance; herbicide resistance; transgenic plant;		
XX	expression construct; enhancer element; ds.		
OS	Oryza sativa.		
XX			
PN	MO20006748-A1.		
FD			
XX	09-NOV-2000.		
PF	20-APR-2000; 2000MO-GB001573.		
XX			
PR	29-APR-1999; 99GB-00009968.		
PR	29-JUL-1999; 99GB-00017834.		
PR	29-JUL-1999; 99GB-00017839.		
PR	29-JUL-1999; 99GB-00017840.		
PR	29-JUL-1999; 99GB-00017846.		
PR	29-JUL-1999; 99GB-00017847.		
PR	21-DEC-1999; 99GB-00030200.		
PR	21-DEC-1999; 99GB-00030204.		
PR	21-DEC-1999; 99GB-00030207.		
PR	21-DEC-1999; 99GB-00030209.		
PR	21-DEC-1999; 99GB-00030213.		
PA	(ZENE ) ZENECA LTD.		
XX			
PI	Hawkes TR, Warner SAJ, Andrews CJ, Bachoo S, Pickerill AP;		
DR	WPI, 2000-687544/67.		
XX			
PT	Novel polynucleotide encoding 5-enolpyruvylshikimate phosphate synthase,		
PT	used to produce transgenic plants e.g. banana, wheat, maize or rice,		
PT	having resistance or tolerance to glyphosate herbicide.		
XX			
PS	Claim 18; Page 56; 87pp; English.		
XX			
CC	The invention relates to rice 5-enolpyruvylshikimate phosphate synthase		
CC	(BPSPS) genomic DNA (AAC87188). The invention also relates to an		
CC	expression cassette comprising, in the 5'-3' direction, one or more		
CC	transcriptional enhancer elements selected from AAC87190-C87196), the		
CC	rice BPSPS promoter, genomic DNA encoding a rice BPSPS chloroplast		
CC	transit peptide, genomic DNA encoding a BPSPS protein modified such that		
CC	it is resistant to glyphosate (AAC87189), and a transcriptional		
CC	terminator. The glyphosate resistant BPSPS contins a region (AAB29793)		
CC	containing two amino acid substitutions relative to the corresponding		
CC	wild-type region (AAB29792). The invention also encompasses plant genomic		
CC	BPSPS sequences identified via screening with a rice BPSPS intronic		
CC	sequence, vectors and host plant cells comprising a nucleic acid sequence		
CC	of the invention; transgenic plants (and tissues and seeds thereof)		
CC	comprising a nucleic acid sequence of the invention, optionally further		
CC	transformed with a DNA encoding an insect, fungal, viral, bacterial,		

CC	nematode, stress or herbicide resistance protein; and methods of
CC	producing the transgenic plants of the invention. The nucleic acids and
CC	constructs of the invention are used to produce a wide variety of
CC	morphologically normal, glyphosate resistant plants. The glyphosate
CC	resistant plants produced are particularly maize, soybean, cotton,
CC	sugarcane and canola, but also other field crops, fruits and vegetables,
CC	turf and forage grasses and nut-producing plants. The plants are
CC	optionally resistant to insects, fungi, viruses, bacteria, nematodes,
CC	stress, desiccation and/or other herbicides. They can be used in the
CC	production of a herbicidal target for the high throughput in vitro
CC	screening of potential herbicides. The present sequence represents an
CC	enhancer element which may be used in the rice EPSPS expression cassette
CC	of the invention
XX	
SO	Sequence 898 BP; 320 A; 166 C; 137 G; 275 T; 0 U; 0 Other;
Query Match	18.3%; Score 402; DB 3; Length 898;
Best Local Similarity	99.3%; Pred. No. 2,le-176;
Matches	862; Conservative 0; Mismatches 2; Indels 4; Gaps 2
Dy	33 CTAACCTAACATATAGGGAAGCGTGTCTAAATATAAATGAGACCTTATATAGTAGCGC 92
Db	34 CTAACCTAACATATAGGGAAGCGTGTCTAAATATAAATGAGACTTATATAGTAGCGC 93
Oy	93 TGATPACTAGCACTATGTAAAGAAAACTCATCCACTCTATTAGTGCAATCGGGCTAAA 152
Dd	94 TGATPACTAGCACTATGTAAAGAAAACTCATCCACTCTATTAGTGGAATCGGGCTAAA 153
Oy	153 TAAAAAAGACGCGTACACTAGTTTCGTTTTCTTAGTAAATTAAGTGGGAAAAATGAATC 212
Dd	154 TAAAAAAGACGCGTACACTAGTTTCGTTTTCTTAGTAAATTAAGTGGGAAAAATGAATC 213
Oy	213 ATTATGTCTTGAATATACGTTGCATCTCTGTGATGATGAAGTTAAATTAATTCGAGGTAGCC 272
Dd	214 ATTATGTCTTGAATATACGTTGCATCTCTGTGATGATGAAGTTAAATTAATTCGAGGTAGCC 273
Oy	273 ATAAATGTCAACAACCTCTCTTGAATTAAGAAAACTTTTCTAGCTGAACCTCAATGGGTAA 332
Dd	274 ATAAATGTCAACAACCTCTCTTGAATTAAGAAAACTTTTCTAGCTGAACCTCAATGGGTAA 333
Oy	333 AGAGAAGATTTTTTTTTTAAAAAAAATAGAAATGAAGATATCTGGAAGTATCGGCAAG 392
Dd	334 AGAGAAGATTTTTTTTTT--AAAAAAAATAGATGAAGATATCTGGAAGTATCGGCAAG 390
Oy	393 ATTTPAACATATATTAATTAATTTAATTTAGTTTGCACTTCGTTATATCGACGCTCAATTA 452
Dd	391 ATTTPAACATATATTAATTAATTTAATTTAGTTTGCACTTCGTTATATCGACGCTCAATTA 450
Oy	453 AGGACATGCTTACTCCATCTCAATTTTATTTAGTAATTAAGCAAATGACCTTATTTT 512
Dd	451 AGGACATGCTTACTCCATCTCAATTTTATTTAGTAATTAAGCAAATGACCTTATTTT 510
Oy	513 TATTATTTATCTTTTTTGATTAAGTAGCAAGGTACTTAAGCACACCTTTTGCTCAGT 572
Dd	511 TATTATTTATCTTTTTTGATTAAGTAGCAAGGTACTTAAGCACACCTTTTGCTCAGT 570
Oy	573 GCATGTGAGTAGGACCTCCCTC-AATACGTTCAACTAGGACACATCTCCAATTAATCACT 631
Dd	571 GCATGTGAGTAGGACCTCCCTCAATTAAGCGTTCAACTAGGACACATCTCTTAATTAATCACT 630
Oy	632 CGCCTATTATTAATACATTAGGTAGCAATATCTGAATTCAGACACTTCAACATCACAGAC 691
Dd	631 CGCCTATTATTAATACATTAGGTAGCAATATCTGAATTCAGACACTTCAACATCACAGAC 690
Oy	692 CACTTTTATATATATCTTAATATCAAAAAATTAATTTTACAGATATGCAATGAAGATATGA 751
Dd	691 CACTTTTATATATATCTTAATATCAAAAAATTAATTTTACAGATATGCAATGAAGATATGA 750
Oy	752 AACGACATATTAAGTTTTTCAACATCAAAAAAAAAGAAATTTTGCTGTCGCCGAGACG 811
Dd	751 AACGACATATTAAGTTTTTCAACATCAAAAAAAAAGAAATTTTGCTGTCGCCGAGACG 810
Oy	812 CCATCTCCATATTTGGGACACAGGACCAACAAGTGTGCTGCCACAGAACCAACCAC 871



Db 66 GCGACCGCCTTCT 78

## RESULT 10

ADK59227  
ID ADK59227 standard; DNA; 725 BP.

AC ADK59227;

DT 06-MAY-2004 (first entry)

DE Plant DNA sequence which confers altered metabolic characteristic #6610.

KW altered metabolic characteristic; plant; acid metabolism;

KW alcohol metabolism; fatty acid metabolism;

KW branched fatty acid metabolism; alkaloid metabolism;

KW amino acid metabolism; ester metabolism; glyceride metabolism;

KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;

KW terpene metabolism; isoprenoid metabolism; alkene metabolism;

KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;

KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.

XX Unidentified.

OS WO2003020936-A1.

PN 13-MAR-2003.

PR 30-AUG-2002; 2002WO-US027884.

PF 31-AUG-2001; 2001US-0316471P.

XX (DOWC ) DOW CHEM CO.

PA (DOWC ) DOW AGROSCIENCES LLC.

PI Weglarz T, Gachotte D, Blakelee B, McCreary DA, Pell RJ;

PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;

XX WPI; 2003-313091/30.

PS Claim 1: SEQ ID NO 6610; 2576bp; English.

XX The invention comprises DNA sequences which confer an altered metabolic

CC characteristic when they are expressed in a plant. The DNA sequences of

CC the invention are useful for producing plants with an altered metabolic

CC characteristic, such as: altered acid metabolism, alcohol metabolism,

CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other

CC base metabolism, altered amino acid metabolism, altered ester metabolism,

CC altered glyceride metabolism, altered phenolic metabolism, altered

CC carbohydrate metabolism, altered sterol, oxygenated terpene, or

CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon

CC metabolism, ketone or quinone metabolism. The DNA sequences of the

CC invention may be used to provide disease resistance in a plant and gene

CC shuffling or sexual PCR procedures. The present nucleic acid represents a

CC DNA sequence of the invention.

Db 67 GCGACCGCCTTCT 79

## RESULT 11

ADD17562  
ID ADD17562 standard; DNA; 782 BP.

AC ADD17562;

DT 15-JAN-2004 (first entry)

DE DNA (SeqID 1630) that confers an altered visual phenotype in plants.

KW ds; visual phenotype; plant; architecture; leaf surface; chlorotic;

KW bleaching; etching; wet leaf; stunting; elongation; texture;

KW agronomic trait; growth regulation; dwarf variety; insect resistance;

KW heat stress; transgenic.

XX Unidentified.

OS WO2003020741-A1.

PN 13-MAR-2003.

PR 30-AUG-2002; 2002WO-US027880.

PF 31-AUG-2001; 2001US-0316326P.

XX (DOWC ) DOW CHEM CO.

PA (DOWC ) DOW AGROSCIENCES LLC.

PI Crosley R, Skokut T, Ruegger M, Larrinua I, Shukla V;

XX WPI; 2003-30858/29.

PS Claim 1: SEQ ID NO 1630; 517bp; English.

XX This invention relates to the identification and isolation of novel

CC nucleic acid molecules that confer altered visual phenotypes in plants.

CC Specifically, it refers to modifications of plant architecture and/or

CC leaf surface features in plants, such as chlorotic, bleaching, etching,

CC wet leaf, stunting, elongation and texture phenotypes, which are thought

CC will be agronomic traits beneficial to the farmer. As such, these novel

CC phenotypes can affect growth regulation i.e. useful for creating dwarf

CC varieties, exhibit resistance to insects or heat stress, confer changes

CC in pigment content such that plants have enhanced vitamin production or

CC delayed senescence and also for example produce plants that control the

CC production of ethylene. Furthermore, the present invention comprises

CC generating transgenic plants, as well as reproducibly altering the visual

CC phenotype of plant seeds, plant tissues and plant cells containing the

CC polynucleotides described herein. This polynucleotide is a homologue of a

CC DNA sequence that confers an altered visual phenotype when expressed in

CC plants, the method of the invention.

XX Sequence 782 BP; 216 A; 190 C; 179 G; 197 T; 0 U; 0 Other;

XX Query Match 3.3%; Score 73; DB 10; Length 782;

Db 67 GCGACCGCCTTCT 79

## RESULT 11

ADD17562  
ID ADD17562 standard; DNA; 782 BP.

AC ADD17562;

DT 15-JAN-2004 (first entry)

DE DNA (SeqID 1630) that confers an altered visual phenotype in plants.

KW ds; visual phenotype; plant; architecture; leaf surface; chlorotic;

KW bleaching; etching; wet leaf; stunting; elongation; texture;

KW agronomic trait; growth regulation; dwarf variety; insect resistance;

KW heat stress; transgenic.

XX Unidentified.

OS WO2003020741-A1.

PN 13-MAR-2003.

PR 30-AUG-2002; 2002WO-US027880.

PF 31-AUG-2001; 2001US-0316326P.

XX (DOWC ) DOW CHEM CO.

PA (DOWC ) DOW AGROSCIENCES LLC.

PI Crosley R, Skokut T, Ruegger M, Larrinua I, Shukla V;

XX WPI; 2003-30858/29.

PS Claim 1: SEQ ID NO 1630; 517bp; English.

XX This invention relates to the identification and isolation of novel

CC nucleic acid molecules that confer altered visual phenotypes in plants.

CC Specifically, it refers to modifications of plant architecture and/or

CC leaf surface features in plants, such as chlorotic, bleaching, etching,

CC wet leaf, stunting, elongation and texture phenotypes, which are thought

CC will be agronomic traits beneficial to the farmer. As such, these novel

CC phenotypes can affect growth regulation i.e. useful for creating dwarf

CC varieties, exhibit resistance to insects or heat stress, confer changes

CC in pigment content such that plants have enhanced vitamin production or

CC delayed senescence and also for example produce plants that control the

CC production of ethylene. Furthermore, the present invention comprises

CC generating transgenic plants, as well as reproducibly altering the visual

CC phenotype of plant seeds, plant tissues and plant cells containing the

CC polynucleotides described herein. This polynucleotide is a homologue of a

CC DNA sequence that confers an altered visual phenotype when expressed in

CC plants, the method of the invention.

XX Sequence 782 BP; 216 A; 190 C; 179 G; 197 T; 0 U; 0 Other;

XX Query Match 3.3%; Score 73; DB 10; Length 782;



RESULT 12  
ADJ39051  
ID ADJ39051 standard; cDNA; 808 BP.  
XX  
AC ADJ39051;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Plant cDNA #51.  
XX  
KM Plant; gene; ss; transcription; plant genome augmentation; cereal;  
KM soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;  
KM maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;  
KM stress tolerance; salt tolerance; cold tolerance; drought tolerance;  
KM plant nutrition; apical dominance; dwarfism; early flowering; antiviral;  
KM antifungal.  
XX  
OS Eukaryota.  
XX  
PN US2004016025-A1.  
XX  
PD 22-JAN-2004.  
XX  
PF 26-SEP-2002; 2002US-00260238.  
XX  
PR 26-SEP-2001; 2001US-0325277P.  
PR 26-SEP-2001; 2001US-0325448P.  
PR 04-APR-2002; 2002US-0370620P.  
XX  
PA (BUDW/) BUDWORTH P.  
PA (MOUG/) MOUGHAMER T.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GORE/) GORE S A.  
PA (KARA/) KARAGIRI F.  
PA (KEPP/) KEPPS J.  
PA (PROV/) PROVART N.  
PA (RICK/) RIQUE D.  
PA (ZHUT/) ZHU T.  
XX  
PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;  
PI Goff SA, Katagiri F, Kreps J, Provart N, Rique D, Zhu T;  
XX  
DR WPI; 2004-190374/18.  
XX  
PT New rice promoter, useful for manipulating crop plants to alter or  
PT improve phenotypic characteristics, e.g. produce large quantities of oil  
PT or proteins, resistance to insecticides, virus or fungi, stress tolerance  
PT or high nutritional value.  
XX  
PS Claim 68; SEQ ID NO 51; 230pp; English.  
XX  
CC The invention relates to plant nucleotide sequences that direct seed-,  
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential  
CC or constitutive transcription of an operatively linked nucleic acid  
CC segment. The invention also relates to a method for augmenting a plant  
CC genome and a method of identifying a gene, where its expression is  
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive  
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,  
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,  
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they  
CC encode are useful for manipulating crop plants to alter or improve  
CC phenotypic characteristics, to produce large quantities of oil or  
CC proteins, to incur resistance to insecticides, viruses or fungi, and to  
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants  
CC have a high nutritional value with reduced apical dominance or dwarfism,  
CC early flowering or altered metabolic pathways. This sequence represents a  
CC plant nucleic acid of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification but was obtained in  
CC electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
SQ Sequence 808 BP; 203 A; 198 C; 188 G; 219 T; 0 U; 0 Other;

Query Match 3.3%; Score 73; DB 12; Length 808;  
Best Local Similarity 100.0%; Pred. No. 3.2e-23;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2122 ATACGCTTGTTCTTATGATTCATTCTTGTGCGAGTCTTGATGACTGACACTT 2181  
DB 139 ATACTGCTTGTTCTTATGATTCATTCTTGTGCGAGTCTTGATGACTGACACTT 198

QY 2182 CACGAGCAAGTT 2194  
DB 199 CACGAGCAAGTT 211

RESULT 13  
AAC8379  
ID AAC8379 standard; DNA; 48 BP.  
XX  
AC AAC8379;  
XX  
DT 02-MAR-2001 (first entry)  
XX  
DE Primer GOS5.  
XX  
KM Glyphosate; 5-enolpyruvylshikimate phosphate synthase; EPSPS;  
KM herbicide resistance; ss.  
XX  
OS Synthetic.  
XX  
PN WO200066746-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-GB0015559.  
XX  
PR 29-APR-1999; 99GB-00009971.  
PR 29-APR-1999; 99GB-00009972.  
PR 29-JUL-1999; 99GB-00017837.  
PR 29-JUL-1999; 99GB-00017842.  
PR 21-DEC-1999; 99GB-00030190.  
PR 21-DEC-1999; 99GB-00030206.  
PR 21-DEC-1999; 99GB-00030214.  
PR 21-DEC-1999; 99GB-00030216.  
XX  
PA (ZENB ) ZENECA LTD.  
XX  
PI Hawkes TR, Warner SAJ, Andrews CJ, Bachoo S, Pickerill AP;  
XX  
DR WPI; 2000-679763/66.  
XX  
PT Novel polynucleotide encoding the rice 5-enolpyruvylshikimate phosphate  
PT synthase, used to produce glyphosate tolerant or resistant plants.  
XX  
PS Example 4; Page 15; 85pp; English.  
XX  
CC The present invention relates to a glyphosate resistant rice 5-  
CC enolpyruvylshikimate phosphate synthase (EPSPS) gene. This gene can be  
CC used to produce plant tissue and/or morphologically normal fertile whole  
CC plants which are tolerant or resistant to glyphosate herbicide, and in  
CC the production of a herbicidal target for the high throughput in vitro  
CC screening of potential herbicides  
XX  
SQ Sequence 48 BP; 10 A; 16 C; 11 G; 11 T; 0 U; 0 Other;

Query Match 1.3%; Score 29; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATCGAAAAGTTTCTGACCGTTTTCAC 29  
DB 19 AATCGAAAAGTTTCTGACCGTTTTCAC 47



RESULT 14  
AAC87162  
ID AAC87162 standard; DNA; 48 BP.  
XX  
AC AAC87162;  
XX  
DT 09-MAR-2001 (first entry)  
XX  
DE Rice GOS2 enhancer element PCR primer, SEQ ID NO:17.  
XX  
KM Rice EPSPS; 5-enolpyruvylshikimate phosphate synthase;  
KW glyphosate resistance; herbicide resistance; transgenic plant;  
expression construct; enhancer element; PCR primer; ss.  
XX  
OS Oryza sativa.  
XX  
PN WO200066748-A1.  
PD 09-NOV-2000.  
XX  
PF 20-APR-2000; 2000MO-GB001573.  
XX  
PR 29-APR-1999; 99GB-00009968.  
XX 29-JUL-1999; 99GB-00017834.  
PR 29-JUL-1999; 99GB-00017839.  
XX 29-JUL-1999; 99GB-00017840.  
PR 29-JUL-1999; 99GB-00017845.  
XX 29-JUL-1999; 99GB-00017847.  
PR 21-DEC-1999; 99GB-00030200.  
XX 21-DEC-1999; 99GB-00030204.  
PR 21-DEC-1999; 99GB-00030207.  
XX 21-DEC-1999; 99GB-00030209.  
PR 21-DEC-1999; 99GB-00030213.  
XX  
PA (ZENB ) ZENECA LTD.  
PI Hawkes TR, Warner SAM, Andrews CJ, Bachoo S, Pickering AP;  
XX  
XX WPI; 2000-687544/67.  
XX  
PT Novel polynucleotide encoding 5-enolpyruvylshikimate phosphate synthase,  
PT used to produce transgenic plants e.g. banana, wheat, maize or rice,  
PT having resistance or tolerance to glyphosate herbicide.  
XX  
XX Example 5; Page 16; 87pp; English.  
PS  
XX The invention relates to rice 5-enolpyruvylshikimate phosphate synthase  
XX (EPSPS) genomic DNA (AAC87162). The invention also relates to an  
XX expression cassette comprising, in the 5'-3' direction, one or more  
XX transcripional enhancer elements selected from AAC87190-C87196), the  
XX rice EPSPS promoter, genomic DNA encoding a rice EPSPS chloroplast  
XX transit peptide, genomic DNA encoding a EPSPS protein modified such that  
XX it is resistant to glyphosate (AAC87169), and a transcripional  
XX terminator. The glyphosate resistant EPSPS contains a region (AAB29793)  
XX containing two amino acid substitutions relative to the corresponding  
XX wild-type region (AAB29792). The invention also encompasses plant genomic  
XX EPSPS sequences identified via screening with a rice EPSPS intronic  
XX sequence; vectors and host plant cells comprising a nucleic acid sequence  
XX of the invention; transgenic plants (and tissues and seeds thereof)  
XX comprising a nucleic acid sequence of the invention, optionally further  
XX transformed with a DNA encoding an insect, fungal, viral, bacterial,  
XX nematode, stress or herbicide resistance protein; and methods of  
XX producing the transgenic plants of the invention. The nucleic acids and  
XX constructs of the invention are used to produce a wide variety of  
XX morphologically normal, glyphosate resistant plants. The glyphosate  
XX resistant plants produced are particularly maize, soybean, cotton,  
XX sugarcane and canola, but also other field crops, fruits and vegetables,  
XX turf and forage grasses and nut-producing plants. The plants are  
XX optionally resistant to insects, fungi, viruses, bacteria, nematodes,  
XX stress, desiccation and/or other herbicides. They can be used in the  
XX production of a herbicidal target for the high throughput in vitro  
XX screening of potential herbicides. The present sequence represents a PCR  
XX primer used in an exemplification of the invention

XX  
SQ Sequence 48 BP; 10 A; 16 C; 11 G; 11 T; 0 U; 0 Other;  
Query Match 1.3%; Score 29; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AATCGAAGAGTTCTGCACCGTTTCAC 29  
DB 19 AATCGAAGAGTTCTGCACCGTTTCAC 47  
RESULT 15  
ABL32090  
ID ABL32090 standard; DNA; 12733 BP.  
XX  
AC ABL32090;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Human immune system associated gene SEQ ID NO: 63.  
XX  
KM Human; immune system disease; cytosine methylation; antiasthmatic;  
KW antileukemic; anti-HIV; anticonvulsant; ophthalmological;  
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
KW antileukemic; anti-HIV; anticonvulsant; ophthalmological;  
KW antileukemic; anti-HIV; anticonvulsant; ophthalmological;  
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;  
ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200200928-A2.  
PD 03-JAN-2002.  
XX  
PF 02-JUL-2001; 2001WO-EP007537.  
XX  
PR 30-JUN-2000; 2000DE-01032529.  
XX 01-SEP-2000; 2000DE-01043826.  
XX  
PA (EPIC-) EPIGENOMICS AG.  
XX  
PI Olek A, Piegenbrock C, Berlin K;  
XX  
XX WPI; 2002-130909/17.  
XX  
PT Nucleic acid comprising fragment of chemically modified gene, useful for  
PT diagnosis and treatment of diseases associated with abnormal cytosine  
PT methylation.  
XX  
XX Claim 1; SEQ ID NO 63; 32pp + Sequence Listing; German.  
XX  
XX The present invention provides a number of human immune system associated  
XX genes which are modified by the methylation of cytosines. The sequences  
XX can be used in the diagnosis and treatment of immune system disorders,  
XX including eye diseases such as retinopathy, neovascular glaucoma and  
XX macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
XX leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
XX rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
XX diseases. The present sequence is a gene of the invention  
XX  
SQ Sequence 12733 BP; 3312 A; 295 C; 3342 G; 5784 T; 0 U; 0 Other;  
Query Match 1.2%; Score 27; DB 6; Length 12733;  
Best Local Similarity 100.0%; Pred. No. 0.074;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 333 AAGAGATTTTATTTTAAAAAAA 359  
DB 1915 AAGAGATTTTATTTTAAAAAAA 1941

Search completed: April 21, 2006, 09:46:52  
Job time : 1226 secs

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OM nucleic - nucleic search, using sw model

Run on: April 21, 2006, 09:13:40 ; Search time 8634 Seconds

(without alignments)  
11625.271 Million cell updates/sec

Title: US-10-541-315-1

Sequence: 1 aatccgaagaagttctgcac.....cacttcaccagcaagttc 2195

Scoring table: OJACO\_NUC

Gapop 60.0, Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size: 8

Total number of hits satisfying chosen parameters: 82156240

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hic:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gss1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	465	21.2	894	10 AG832683	AG832683 Oryza sat
C 2	394	17.9	775	9 AQ871933	AQ871933 nbe00458
C 3	291	13.3	716	1 AU075848	AU075848 AU075848
C 4	227	10.3	627	6 CF304397	CF304397 ABR1--04-
C 5	212	9.7	619	6 CF306344	CF306344 HDL1--03-
C 6	203	9.2	585	7 CFK038003	CFK038003 41717rslc
C 7	178	8.1	578	6 CF303311	CF303311 ABR1--01-
C 8	148	6.7	844	7 CR291032	CR291032 CR291032
C 9	147	6.7	848	10 AG871481	AG871481 Oryza sat
C 10	146	6.7	324	6 CF305170	CF305170 ABR1--06-
C 11	121	5.5	210	7 CF993308	CF993308 18211rslc
C 12	106	4.8	479	6 CF278393	CF278393 14ETL--04
C 13	100	4.6	288	6 CF304743	CF304743 ABR1--05-
C 14	90	4.1	295	7 CV731585	CV731585 FLO--05-K
C 15	83	3.8	982	5 BX929024	BX929024 BX929024
C 16	80	3.6	239	7 CK042297	CK042297 43579rslc
C 17	77	3.5	596	6 CF331107	CF331107 NACL--07-
C 18	75	3.4	557	6 CF340566	CF340566 RCL1--08-
C 19	75	3.4	560	6 CF338527	CF338527 RCL1--01-
C 20	75	3.4	677	6 CF339901	CF339901 RCL1--06-
C 21	75	3.4	680	6 CF328175	CF328175 NACL--02-
C 22	74	3.4	472	7 CV733575	CV733575 FLO--08-1

23	74	3.4	539	7 CV724966	CV724966 14SalT--0
24	74	3.4	550	6 CF280385	CF280385 14ETL--07
25	74	3.4	550	6 CF280540	CF280540 14ETL--07
26	74	3.4	552	6 CF319604	CF319604 HD--10-C1
27	74	3.4	559	6 CF277809	CF277809 14ETL--03
28	74	3.4	563	6 CF309066	CF309066 ABR--03-B
29	74	3.4	564	6 CF278675	CF278675 14ETL--04
30	74	3.4	565	6 CF315243	CF315243 HD--04-B1
31	74	3.4	565	6 CF331926	CF331926 NACL--08-
32	74	3.4	566	6 CF281181	CF281181 14ETL--08
33	74	3.4	566	6 CF321214	CF321214 HD--12-G0
34	74	3.4	567	6 CF307781	CF307781 ABR--01-F
35	74	3.4	624	6 CF319251	CF319251 HD--09-L0
36	73	3.3	491	7 CV730436	CV730436 FLO--03-P
37	73	3.3	562	6 CF332013	CF332013 NACL--08-
38	72	3.3	220	6 CF316654	CF316654 HD--06-A1
39	72	3.3	240	6 CF309951	CF309951 ABR--04-F
40	72	3.3	374	6 CF281983	CF281983 14ETL--09
41	72	3.3	438	6 CF276542	CF276542 14ETL--01
42	72	3.3	465	6 CF278096	CF278096 14ETL--01
43	72	3.3	467	6 CF282366	CF282366 14ETL--09
44	72	3.3	468	6 CF278405	CF278405 14ETL--04
45	72	3.3	489	7 CV727881	CV727881 14SalT--0

#### ALIGNMENTS

RESULT 1  
AG832683/c  
LOCUS  
DEFINITION  
BAC clone:K0010A06\_F, genomic survey sequence.  
ACCESSION  
AG832683  
VERSION  
AG832683.1 GI:55298918  
KEYWORDS  
GSS.  
SOURCE  
Oryza sativa (indica cultivar-group)  
ORGANISM  
Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS  
Katagiri,S., Wu,J., Ito,Y., Karasawa,W., Shibata,M., Kanamori,H.,  
Katayose,Y., Namiki,N., Matsumoto,T. and Sasaki,T.  
TITLE  
End Sequencing and Chromosomal in silico Mapping of BAC Clones  
Derived from an indica Rice Cultivar, Kasalath  
JOURNAL  
Breeding Science 54, 273-279 (2004)  
REFERENCE  
AUTHORS  
Sasaki,T., Matsumoto,T. and Wu,J.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (29-OCT-2004) Takuji Sasaki, National Institute of  
Agrobiological Sciences, Rice Genome Research Program, Kannondai  
2-1-2, Tsukuba, Ibaraki, 305-8602, Japan  
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/  
Tel:81-298-38-7441, Fax:81-298-38-7468)

COMMENT  
The orientation of the sequence is from T7 side of the BAC clone.

FEATURES  
source  
1..894  
/organism="Oryza sativa (indica cultivar-group)"  
/mol\_type="genomic DNA"  
/cultivar="Kasalath"  
/db\_xref="taxon:39946"  
/clone="K0010A06\_F"

#### ORIGIN

Query Match 21.2%, Score 465, DB 10, Length 894;  
Best Local Similarity 99.8%; Pred. No. 1,9e-213;  
Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1679 ATTCCCTGTTCTTCGATTTGCTTAGTCCGGAATTTTTCCTCAATATCTTAAAAA 1738  
DB 630 ATTCCCTGTTCTTCGATTTGCTTAGTCCGGAATTTTTCCTCAATATCTTAAAAA 571

QY 1739 GTGACCTTTCTGCTTCACTTCAATGAAATGATTCGTAACAAATATGCTTTTATAGCTTAT 1798  
DB 570 GTTCTTTCTGCTTCACTTCAATGAAATGATTCGTAACAAATATGCTTTTATAGCTTAT 511  
QY 1799 CCGAGCTGATGCTCACTTATAGTAATACCCCTATAGTTAGTCAGAGAAAGACTTAT 1858  
DB 510 CTTAGCTGATGCTCACTTATAGTAATACCCCTATAGTTAGTCAGAGAAAGACTTAT 451  
QY 1859 CCGATTTCTGATCTCCATTTTATATATGAAATGAACTGATGATGATGATGATGAT 1918  
DB 450 CCGATTTCTGATCTCCATTTTATATATGAAATGAACTGATGATGATGATGATGAT 391  
QY 1919 TTGATATATATTTTATATATAGCTTCAACCCCTCATTTATGAGCTGAAAGCTGCAAT 1978  
DB 390 TTGATATATATTTTATATATAGCTTCAACCCCTCATTTATGAGCTGAAAGCTGCAAT 331  
QY 1979 GAACGTCTCCATTTTATGTTTCAAAATTCATGATGATGATGATGATGATGATGAT 2038  
DB 330 GAACGTCTCCATTTTATGTTTCAAAATTCATGATGATGATGATGATGATGATGAT 271  
QY 2039 TCTACCTGTAGAAGTTCTTTTGTATATCTTGAATGCTGCTGATGATGATGATGAT 2098  
DB 270 TCTACCTGTAGAAGTTCTTTTGTATATCTTGAATGCTGCTGATGATGATGATGAT 211  
QY 2099 ATGAGCTGTATATCGGATATGATATCTGCTTCTTATGATGATGATGATGATGAT 2158  
DB 210 ATGAGCTGTATATCGGATATGATATCTGCTTCTTATGATGATGATGATGATGAT 151  
QY 2159 TTCTGTGTAGCTGCTCACTTTCACGAGCAAGTT 2194  
DB 150 TTCTGTGTAGCTGCTCACTTTCACGAGCAAGTT 115

RESULT 2  
LOCUS AO871933/c 775 bp DNA linear GSS 03-NOV-1999  
DEFINITION nbe0045B22r CUGI Rice BAC Library (ECORI) Oryza sativa (japonica  
cultivar-group) genomic clone nbe0045B22r, genomic survey  
sequence.

ACCESSION AO871933  
VERSION AO871933.1 GI:6222384  
KEYWORDS GSS.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 775)  
AUTHORS Wing, R.A. and Dean, R.A.  
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome  
JOURNAL Unpublished (1998)  
COMMENT Contact: Wing RA  
Clemson University Genomics Institute  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Seq primer: GGAAACAGCTATGACATG  
Class: BAC ends  
High quality sequence start: 170  
High quality sequence stop: 311.  
Location/Qualifiers  
1..775  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="genomic DNA"  
/cultivar="japonica"  
/cultivar="Nipponbare"  
/db\_xref="taxon:39947"  
/clone="nbe0045B22r"  
/issue\_type="leaf"  
/lab\_host="E. coli DH10B"  
/clone\_lib="CUGI Rice BAC Library (ECORI)"

FEATURES  
source

## ORIGIN

/note="vector: pBACindigo; Site 1: EcoRI; Site 2: EcoRI;  
Rice is the most important food crop in the world. Half of  
the world population, especially those inhabiting highly  
populated areas of the humid tropics and subtropics, rely  
on rice as their primary source of carbohydrate.  
Monocotyledonous rice is a diploid plant (2n=24) with a  
haploid genome equivalent of 431 Mbp (Arumuganathan and  
Earle, 1991). The relatively small genome of rice, three  
times larger than that of Arabidopsis, makes it suitable  
for genomic studies. In order to facilitate positional  
cloning, physical mapping and genome sequencing of rice,  
we have constructed a BAC library from Oryza sativa.  
Nipponbare variety using EcoRI as the cloning enzyme. The  
library contains 55,296 clones with an average insert size  
of 121 Kb providing approximately 15 haploid genome  
equivalents. The deep coverage allows the isolation of a  
particular sequence with a probability of 99.9%. Three  
high density filters, each containing 18,432 clones  
(doubly spotted), represent the whole library for colony  
screening and can be requested from the Clemson University  
BAC/EST Resource Center (www.genome.clemson.edu)."

Query Match 17.9%; Score 394; DB 9; Length 775;  
Best Local Similarity 100.0%; Pred. No. 4.7e-179; Indels 0; Gaps 0;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 AATGACCTTATATATGAGCGCTGATPACTGATGATGATGATGATGATGATGATGAT 128  
DB 621 AATGACCTTATATATGAGCGCTGATPACTGATGATGATGATGATGATGATGATGAT 562  
QY 129 TACTTATGCGCAATCGGCTTAATTAATAAAGATCGCTCACTGATGTTCCGTTCTTA 188  
DB 561 TACTTATGCGCAATCGGCTTAATTAATAAAGATCGCTCACTGATGTTCCGTTCTTA 502  
QY 189 GTAATTAAGTGGAAATGAATCATTTATGCTTGAATATATGCTTCACTCTGTGAT 248  
DB 501 GTAATTAAGTGGAAATGAATCATTTATGCTTGAATATATGCTTCACTCTGTGAT 442  
QY 249 GAAGTTAAATATATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 308  
DB 441 GAAGTTAAATATATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 382  
QY 309 TTTCTAGCTGAACCTCAATGCGGTAAGAGATATTTTTTTTAAATAAATAATGATGAA 368  
DB 381 TTTCTAGCTGAACCTCAATGCGGTAAGAGATATTTTTTTTAAATAAATAATGATGAA 322  
QY 369 GATATTTGAAGCTATCGGCAAAAGATTTAAACATATATATATATATATATATATAT 428  
DB 321 GATATTTGAAGCTATCGGCAAAAGATTTAAACATATATATATATATATATATATAT 262  
QY 429 CATTGTTATATCGACGCTATTAAGACATGTC 462  
DB 261 CATTGTTATATCGACGCTATTAAGACATGTC 228

RESULT 3  
LOCUS AU075848 716 bp mRNA linear EST 03-APR-2002  
DEFINITION AU075848 Rice mature leaf Oryza sativa (japonica cultivar-group)  
CDNA clone S20385\_1A, mRNA sequence.  
ACCESSION AU075848  
VERSION AU075848.1 GI:5455455  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 716)  
AUTHORS Yamamoto, K. and Sasaki, T.  
TITLE Rice cDNA from mature leaf  
JOURNAL Unpublished (1999)



DEFINITION	HDAl-03-109, g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library 1 (HDAl) Oryza sativa (japonica cultivar-group) cDNA clone HDAl-03-109, mRNA sequence.
ACCESSION	CF306344.1 GI:33678105
VERSION	EST.
KEYWORDS	Oryza sativa (japonica cultivar-group)
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group)
REFERENCE	Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. -K. and Nahm, B. H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
TITLE	Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
JOURNAL	Yongin, Kyeonggi, Korea
COMMENT	Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES	location/Qualifiers
SOURCE	1.. 619 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nackdong" /db_xref="taxon:39947" /clone="HDAl-03-109" /issue_type="callus" /dev_stage="proliferated callus on 2N6 media for 2 weeks" /lab_host="E. coli SOLR" /clone_lib="OSHDA1-overexpressing transgenic rice lambda phage cDNA library 1 (HDAl)" /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."
ORIGIN	
Query Match	9.7%; Score 212; DB 6; Length 619;
Best Local Similarity	99.3%; Pred. No. 7,1e-91;
Matches 432; Conservative	0; Mismatches 2; Indels 1; Gaps 1;
OY	1216 TTGATGTAGAAAGGGGATCTGATCTGTATGATTCCTGTCCTTGATTTGGATATGA 1275
DB	186 TTGATGTAGAAAGGGGATCTGATCTGTATGATTCCTGTCCTTGATTTGGATATGA 245
OY	1276 GGGGTTCTTGATGTGCATGTTATTCGGTTCGGTTGATTAGTAGATGTTTCATTCGT 1335
DB	246 GGGGTTCTTGATGTGCATGTTATTCGGTTCGGTTGATTAGTAGATGTTTCATTCGT 305
OY	1336 CTGAGAGACTTATGAGAAATGAATGTTTAGGGGTACGGAATCTTGCGATTTTGTGAGTA 1395
DB	306 CTGAGAGACTTATGAGAAATGAATGTTTAGGGGTACGGAATCTTGCGATTTTGTGAGTA 365
OY	1396 CCTTTGTTTGAAGTAAATACAGACACCGGTGATTTTTCGTGGTGAATAAAGTACAT 1455
DB	366 CCTTTGTTTGAAGTAAATACAGACACCGGTGATTTTTCGTGGTGAATAAAGTACAT 424
OY	1456 TTGTTTGGTCTCTGATTCGTGTAGTAGTCTTCCTCGATTTTGACGAGCTATCTTGTGTT 1515
DB	425 TTGTTTGGTCTCTGATTCGTGTAGTAGTCTTCCTCGATTTTGACGAGCTATCTTGTGTT 484
OY	1516 ATTCCTTAATGAACAAAATATATCAACTTTGAAGACGGTCCGGTGTATGAGATTGAATG 1575
DB	485 ATTCCTTAATGAACAAAATATATCAACTTTGAAGACGGTCCGGTGTATGAGATTGAATG 544
OY	1576 ATTGATTTCTTAAGCTGTCCAAATTTTGGACGCTGGCTTTGTTTAGATACAGTAGTCCCCA 1635
DB	545 ATTGATTTCTTAAGCTGTCCAAATTTTGGACGCTGGCTTTGTTTAGATACAGTAGTCCCCA 604

OY	1636	TCACGAATTCATGA	1650
Db	605	TCACGAATTCATCA	619
RESULT 6			
CX038003			
LOCUS			
DEFINITION	CX038003	585 bp	mRNA linear EST 04-FEB-2005
	cdna library Oryza sativa cv. 93-11 cllering whole plant		
ACCESSION	CX038003		
VERSION	CX038003.1	GI:58609970	
KEYWORDS	EST.		
SOURCE	Oryza sativa		
ORGANISM	Oryza sativa		
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.		
AUTHORS	Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W., Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X., Zheng, H., Cong, L., Lin, L., Yin, D., Geng, J., Li, G., Shi, U., Liu, J., Lv, H., Li, J., Wang, J., Deng, Y., Kan, L., Shi, X., Wang, X., Wu, Q., Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z., Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, D., Chen, P., Wu, S., and Liu, J.		
TITLE	The Genomes of Oryza sativa: A History of Duplications		
JOURNAL	PLoS Biol. 3 (2), e38 (2005)		
PUBMED	15685292		
COMMENT	Contact: Yan Zhou Bioinformatics Department Hangzhou Genomics Institute No.51 Zhijiang Road, Hangzhou 310008, China Tel: 86-571-56805886 Fax: 86-571-56805884 Email: zhouyan@genomics.org.cn Seq primer: M13 Forward High quality sequence stop: 585 POLYA=NO.		
FEATURES			
source	Location/Qualifiers		
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	/organism="Oryza sativa"		
	/mol_type="mRNA"		
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	/cissue_type="whole plant"		
	/dev_stage="cllring"		
	/clone_lib="Oryza sativa cv. 93-11 cllering whole plant cdna library"		
ORIGIN			
Query Match	9.2%; Score 203; DB 7; Length 585;		
Best Local Similarity	100.0%; Pred. No. 1,6e-86;		
Matches 203; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
OY	1167	CCCTCGGTTCTTGAGATTATGTCTTAAAGTTGGTAGAGGGGTTGATTAG	1226
Db	143	CCCTCGGTTCTTGAGATTATGTCTTAAAGTTGGTAGAGGGGTTGATTAGC	202
OY	1227	AAAAGGATCTGTAATCTGTATGATTCCTGTTCTTGATTGGATAGAGGGTCTTGA	1286
Db	203	AAAAGGATCTGTAATCTGTATGATTCCTGTTCTTGATTGGATAGAGGGTCTTGA	262
OY	1287	TGTTGCATGTATTCGGTTCCGTTGATTAGTAGTAGGTTTCAATGCTCTGAGAGACTC	1346
Db	263	TGTTGCATGTATTCGGTTCCGTTGATTAGTAGTAGGTTTCAATGCTCTGAGAGACTC	322
OY	1347	TATGAAATGAATGCTTTAGG	1369
Db	323	TATGAAATGAATGCTTTAGG	345

RESULT 7  
CF303311 578 bp mRNA linear EST 15-AUG-2003  
LOCUS ABF1--01-016-g1 ABF1-overexpressing transgenic rice lambda phage  
DEFINITION cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA  
clone ABF1--01-016, mRNA sequence.  
ACCESSION CF303311 GI:33675072  
VERSION CF303311.1  
KEYWORDS Oryza sativa (japonica cultivar-group)  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriophytaceae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 578)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.T., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
FEATURES  
source  
1..578  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="ABF1-01-016"  
/rissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli SOLR"  
/clone\_lib="ABF1-overexpressing transgenic rice lambda  
phage cDNA library (ABF1)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; Leaf was dried for 2hrs. cDNA was inserted into  
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end  
with XhoI site. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

ORIGIN  
Query Match 8.1%; Score 178; DB 6; Length 578;  
Best Local Similarity 99.3%; Pred. No. 2.1e-74;  
Matches 398; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
1216 TTGAGCTTGGAGAAAGGGATCTGATCTGATGATTCGCTTCTGGATTGGAGTAGA 1275  
|||||  
179 TTGAGTGAAGAAAGGGATCTGATCTGATGATTCGCTTCTGGATTGGAGTAGA 238  
|||||  
1276 GGGGTTCTGATGATGATGATTCGCTTCTGGATTGGATTAGTAGATGATTCATCGT 1335  
|||||  
239 GGGGTTCTGATGATGATGATTCGCTTCTGGATTAGTAGATGATTCATCGT 298  
|||||  
1336 CTGAGAGCTTATGAGAAATGAATGTTAGGGTACGGAATCTTCCGATTGTTGAGTA 1395  
299 CTGAGAGCTTATGAGAAATGAATGTTAGGGTACGGAATCTTCCGATTGTTGAGTA 358  
|||||  
1396 CTTTGTGTTGAGTAAATCGAGACCGGTGATTTGCTGGTATTAATAAGTACAT 1455  
|||||  
359 CTTTGTGTTGAGTAAATCGAGACCGGTGATTTGCTGGTATTAATAAGTACAT 417  
|||||  
1456 TTGTTGTCCTGATTCGTGATGATGCTTCTCGATTGACGAAGCTATCCTTTGTT 1515  
418 TTGTTGTCCTGATTCGTGATGATGCTTCTCGATTGACGAAGCTATCCTTTGTT 477  
|||||  
1516 ATTCCCTATTGAACAAATAATCAACTTTGAAGACGGTCCGTTGATGAGATTGAATG 1575  
478 ATTCCCTATTGAACAAATAATCAACTTTGAAGACGGTCCGTTGATGAGATTGAATG 537  
|||||

OY 1576 ATTGATTTCTTAAGCCTGTCCAAAATTTCCGACCTGGCTTGT 1616  
|||||  
DB 538 ATTGATTTCTTAAGCCTGTCCAAAATTTCCGACCTGGCTTGT 578  
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RESULT 8  
CR291032 844 bp mRNA linear EST 27-FEB-2004  
LOCUS CR291032  
DEFINITION Y604h07p5, mRNA sequence.  
ACCESSION CR291032 GI:44677598  
VERSION CR291032.1  
KEYWORDS Oryza sativa  
SOURCE Oryza sativa  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriophytaceae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 844)  
AUTHORS Han,B., Feng,Q., Huang,Y.C., Yang,K., Li,Y., Guan,J.P., Zhu,J.J.,  
Zhao,Q., Hu,X., Liu,Y.L., Mu,J., Yu,Z., Chen,L., Fan,D.L.,  
Weng,Q.J., Zhang,L., Lu,Y.Q., Yu,S.L., Liu,X.H., Lu,T.T.,  
Zhang,Y.J., Lu,Y., Li,C., Li,T., Zhang,Y., Hu,H., Jia,P.X.,  
Zhang,L., Lan,L.F., Chen,W., Wu,S.A. and Xue,Y.B.  
TITLE Rice cDNA EST clone  
JOURNAL Unpublished (2003)  
COMMENT Contact: Han Bin  
National Center for Gene Research  
Chinese Academy of Sciences  
500# Cao Bao Road, Shanghai 200233, China  
Email: bhan@ncgr.ac.cn  
Clone requests: bhan@ncgr.ac.cn  
This is rice cDNA est clone  
Web site: http://www.ncgr.ac.cn.  
Location/Qualifiers  
FEATURES  
source  
1..844  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/db\_xref="taxon:4530"  
/clone="Y604h07p5"  
/clone\_lib="Oryza sativa library (Han B)"

ORIGIN  
Query Match 6.7%; Score 148; DB 7; Length 844;  
Best Local Similarity 100.0%; Pred. No. 7e-60;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
947 GAGGAGAGCAAGAAACCAAGATCTCTCTCCATCTATAATTCCTCCCTT 1006  
24 GAGGAGAGCAAGAAACCAAGATCTCTCTCCATCTATAATTCCTCCCTT 83  
OY 1007 TTCCCTCTCTATATAGAGGATCCAGCCCAAGAGGAGAGCAACAGACACCGG 1066  
DB 84 TTCCCTCTCTATATAGAGGATCCAGCCCAAGAGGAGAGCAACAGACACCGG 143  
OY 1067 ACTAGCAGAGCGGAGCGGACCGCTTCT 1094  
DB 144 ACTAGCAGAGCGGAGCGGACCGCTTCT 171  
|||||

RESULT 9  
AG871481 848 bp DNA linear GSS 03-NOV-2004  
LOCUS AG871481  
DEFINITION Oryza sativa (indica cultivar-group) genomic DNA, BAC end sequence,  
BAC clone:K0245F03\_R, genomic survey sequence.  
ACCESSION AG871481  
VERSION AG871481.1 GI:55337716  
KEYWORDS GSS  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;





/issue\_type="whole plant"  
/dev\_stage="tillering"  
/clone\_1ib="Oryza sativa cv. Lyp9 tillering whole plant  
cDNA library"

## ORIGIN

Query Match 5.5%; Score 121; DB 7; Length 210;  
Best Local Similarity 100.0%; Pred. No. 9.3e-47;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 974 CTCCTCTCCCATCTATAATTCCTCCCTTTCCCTCTCTATATAGAGGACATCA 1033

Db 9 CTCCTCTCCCATCTATAATTCCTCCCTTTCCCTCTCTATATAGAGGACATCA 68

Oy 1034 ACCCAAGAGAGAGAGAGACCAAGAGACGACCTAGAGAAAGCCGAGCGGCTTC 1093

Db 69 ACCCAAGAGAGAGAGAGACCAAGAGACGACCTAGAGAAAGCCGAGCGGCTTC 128

Oy 1094 T 1094

Db 129 T 129

## RESULT 12

CF278393 479 bp mRNA linear EST 14-AUG-2003

LOCUS 14ETL--04-E15.g1 Rice etiolated leaf plasmid cDNA library (14ETL)

DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-E15,

mRNA sequence.

ACCESSION CF278393.1 GI:33655779

VERSION CF278393.1

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

SpERMatoPhyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 479)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. 479

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="14ETL--04-E15"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_1ib="Rice etiolated leaf plasmid cDNA library

(14ETL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

## ORIGIN

Query Match 4.8%; Score 106; DB 6; Length 479;

Best Local Similarity 100.0%; Pred. No. 1.6e-39;

Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 986 TCTATAAATTCCTCCCTCTCTCTATATAGAGGACATCAAGCAAGAG 1045

Db 83 TCTATAAATTCCTCCCTCTCTCTATATAGAGGACATCAAGCAAGAG 142

Oy 1046 GGAGAGCACCAAGAGACGCGCTAGAGAGCCGACGCGCT 1091

Db 143 GGAGAGCACCAAGAGACGCGCTAGAGAGCCGACGCGCT 188

## RESULT 13

CF304743

LOCUS

DEFINITION

ABF1--05-N05.g1 ABF3-overexpressing transgenic rice lambda phage

cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA

clone ABF1--05-N05, mRNA sequence.

CF304743

ACCESSION

CF304743.1 GI:33676504

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. 288

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="ABF1--05-N05"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli SOLR"

/clone\_1ib="ABF3-overexpressing transgenic rice lambda

phage cDNA library (ABF1)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; Leaf was dried for 2hrs. cDNA was inserted into

lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end

with XhoI site. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

## ORIGIN

Query Match 4.6%; Score 100; DB 6; Length 288;

Best Local Similarity 100.0%; Pred. No. 1.4e-36;

Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1216 TTGATGTAGAGAAAGGATCGTATCTGTATGATTCCTGTTGGATTGGATGA 1275

Db 179 TTGATGTAGAGAAAGGATCGTATCTGTATGATTCCTGTTGGATTGGATGA 238

Oy 1276 GGGGTTCTTGATGTGATGTTATCGTTCGGTTGATTGA 1315

Db 229 GGGGTTCTTGATGTGATGTTATCGTTCGGTTGATTGA 278

## RESULT 14

CV731585

LOCUS

DEFINITION

ABF1--05-K23.b1 Rice flower lambda phage cDNA library (FLO) Oryza

sativa (japonica cultivar-group) cDNA clone FLO--05-K23, mRNA

sequence.

CV731585

ACCESSION

CV731585.1 GI:55436839

VERSION





OY	333	AGAGAGATTTTTTTTTTAAAAAATAATGAATGAAGATTTCTGAAACGATCGGCAAG	3392
Db	334	AGAGAGATTTTTTTTTT---AAAAAATGAAATGAAGATTTCTGAAACGATCGGCAAG	3390
OY	393	ATTTAACATATATATATATATATTTATATAGTTTGTGCATTCGTTATATCGCACGTCATTA	4522
Db	391	ATTTAACATATATATATATATATTTTATAGTTTGTGCATTCGTTATATCGCACGTCATTA	4500
OY	433	AGGACATGCTTACTCTCATCTCAATTTTTTATTTAGTATTAAGAACAATTGACTTATTTT	5122
Db	451	AGGACATGCTTACTCTCATCTCAATTTTTTATTTAGTATTAAGAACAATTGACTTATTTT	5100
OY	513	TATTAATTATCTTTTTTGGATTAGATGCAAGGTACTTAAGCACACACTTTGTGCTCATGT	5722
Db	511	TATTAATTATCTTTTTTGGATTAGATGCAAGGTACTTAAGCACACACTTTGTGCTCATGT	5700
OY	573	GCATGTGTGAGTGACACTCTCTC-ATAACAGTTTCAACTAGGACACATCTTCCAAATATCACT	6312
Db	571	GCATGTGTGAGTGACACTCTCTCAATACAGTTTCAACTAGGACACATCTCTAATATCACT	6300
OY	632	CGCCTAATTTAATACATTTTAGTNGTGCATATCTGAATTCAAGCACTTCAACATCAACAAC	6912
Db	631	CGCCTAATTTAATACATTTTAGTNGTGCATATCTGAATTCAAGCACTTCAACATCAACAAC	6900
OY	692	CACCTTTTAATATATCTAATAAATACAAAAAATATTTTACAGATATAGACGAATAAGTATGA	7512
Db	691	CACCTTTTAATATATCTAATAAATACAAAAAATATTTTACAGATATAGACGAATAAGTATGA	7500
OY	752	AACGAACCTTATAGGTTTTTTCACATACAAAAAAAAGATTTTCTCGTGGCGAGCG	8112
Db	751	AACGAACCTTATAGGTTTTTTCACATACAAAAAAGATTTTCTCGTGGCGAGCG	8100
OY	812	CCAATCTCCCATATTTGGGACACACAGGCAACAACAGAGTGGCTGCCACAGAAACAACCCAC	8712
Db	811	CCAATCTCCCATATTTGGGACACACAGGCAACAACAGAGTGGCTGCCACAGAAACAACCCAC	8700
OY	872	AAAAAACAATGATCTTAACGAGAGACACG	899
Db	871	AAAAAACAATGATCTTAACGAGAGACACG	898

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RESULT 2
US-10-012-070A-17
Sequence 17, Application US/10012070A
Patent No. 6867293
GENERAL INFORMATION:
APPLICANT: Hawkes, Timothy
APPLICANT: Warner, Simon
APPLICANT: Andrews, Christopher
APPLICANT: Bachoo, Satvinder
APPLICANT: Pickrell, Andrew
TITLE OF INVENTION: Herbicide Resistant Plants
FILE REFERENCE: 50490/UST
CURRENT APPLICATION NUMBER: US/10/012,070A
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: PCT/GB00/01573
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 48
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:primer
US-10-012-070A-17

```

Query Match	1.3%	Score 29;	DB 3;	Length 48;
Best Local Similarity	100.0%;	Pred. No. 0.0063;		
Matches 29;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1 AATCGAAAAGTTTCTGCACCGTTTTCAC	29		

[illegible]

```

RESULT 4
US-10-349-782-6/c
: Sequence 6, Application US/10349782
: Patent No. 6955882
: GENERAL INFORMATION:
: APPLICANT: Yves Hatzfeld
: APPLICANT: Valerie Marie-No. 695588211e Frankard
: APPLICANT: Anne-Marie Droual
: TITLE OF INVENTION: Method for easy cloning and selection of chimeric DNA molecules
: FILE REFERENCE: 1187-15
: CURRENT APPLICATION NUMBER: US/10/349,782
: CURRENT FILING DATE: 2003-01-23
: PRIOR APPLICATION NUMBER: EP 02075373.7
: PRIOR FILING DATE: 2002-01-23
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 6
: LENGTH: 22
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Primer 2432 (N1)
US-10-349-782-6

```

```

Query Match          1.0%; Score 22; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 8 9;
Matches      22; Conservative    0; Mismatches     0; Indels     0; Gaps     0;

OY      2174 GCCACTTTCACCGCAAAAGTTC 2195
        |||||||
Db       22   GCCACTTTCACCGCAAAAGTTC 1

RESULT 5
US-10-012-070A-1B/C
; Sequence 1B, Application US/10012070A
```

```
; Patent No. 6867293
; GENERAL INFORMATION:
; APPLICANT: Hawkes, Timothy
; APPLICANT: Warner, Simon
; APPLICANT: Andrews, Christopher
; APPLICANT: Bachoo, Savinder
; APPLICANT: Pickett, Andrew
; TITLE OF INVENTION: Herbicide Resistant Plants
; FILE REFERENCE: 50490/UST
; CURRENT APPLICATION NUMBER: US/10/012,070A
; PRIOR FILING DATE: 2001-10-29
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 18
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer
US-10-012-070A-18

Query Match          1.0%; Score 22; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      878 CGATGATCTAACGAGAGACG 899
DB      36 CGATGATCTAACGAGAGACG 15

RESULT 6
US-09-949-016-13185/C
; Sequence 13185, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13185
; LENGTH: 251769
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13185

Query Match          1.0%; Score 22; DB 3; Length 251769;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      709 AAAATACAAAAAATATTATTTAC 730
DB      119547 AAAATACAAAAAATATTATTTAC 119526

RESULT 7
US-09-949-016-13186/C
; Sequence 13186, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

```
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13186
; LENGTH: 251769
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13186

Query Match          1.0%; Score 22; DB 3; Length 251769;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      709 AAAATACAAAAAATATTATTTAC 730
DB      119547 AAAATACAAAAAATATTATTTAC 119526

RESULT 8
US-09-949-016-13187/C
; Sequence 13187, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13187
; LENGTH: 266748
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13187

Query Match          1.0%; Score 22; DB 3; Length 266748;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      709 AAAATACAAAAAATATTATTTAC 730
DB      119512 AAAATACAAAAAATATTATTTAC 119491

RESULT 9
US-09-949-016-13188/C
; Sequence 13188, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
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;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 13188  
;; LENGTH: 266748  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-13188

Query Match 1.0%; Score 22; DB 3; Length 266748;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 709 AAAATTCAGAAAAATATTTTAC 730  
DB 119512 AAAATTCAGAAAAATATTTTAC 119491

RESULT 10  
US-09-423-233-18  
;; Sequence 18, Application US/09423233  
;; Patent No. 6372430  
;; GENERAL INFORMATION:  
;; APPLICANT: The Government of the United States of America as  
;; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and  
;; FILE REFERENCE: 03063-0341MP  
;; CURRENT APPLICATION NUMBER: US/09/423,233  
;; PRIOR FILING DATE: 2000-06-27  
;; NUMBER OF SEQ ID NOS: 61  
;; SOFTWARE: Patentin Ver. 2.0  
;; SEQ ID NO 18  
;; LENGTH: 360  
;; TYPE: DNA  
;; ORGANISM: Rhizopus circinans  
US-09-423-233-18

Query Match 1.0%; Score 21; DB 3; Length 360;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 339 ATATTTTTTTTAAAAAAA 359  
DB 125 ATATTTTTTTTAAAAAAA 145

RESULT 11  
US-09-533-559-1048  
;; Sequence 1048, Application US/09533559  
;; Patent No. 6902887  
;; GENERAL INFORMATION:  
;; APPLICANT: Randy M. Berka  
;; APPLICANT: Michael W. Rey  
;; APPLICANT: Jeffrey R. Shuster  
;; APPLICANT: Sakari Kauppinen  
;; APPLICANT: Peter Bjarke Olsen  
;; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
;; FILE REFERENCE: 5849-200-US  
;; CURRENT APPLICATION NUMBER: US/09/533,559  
;; PRIOR FILING DATE: 2000-03-22  
;; EARLIER APPLICATION NUMBER: 09/273,623  
;; NUMBER OF SEQ ID NOS: 7860  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1048  
;; LENGTH: 487  
;; TYPE: DNA

;; ORGANISM: Fusarium venenatum  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (1)...(487)  
;; OTHER INFORMATION: n = A,T,C or G  
US-09-533-559-1048

Query Match 1.0%; Score 21; DB 3; Length 487;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 TTTTAAAAAAAATAG 362  
DB 31 TTTTAAAAAAAATAG 51

RESULT 12  
US-09-949-016-187814/C  
;; Sequence 187814, Application US/09949016  
;; Patent No. 6812339  
;; GENERAL INFORMATION:  
;; APPLICANT: VENTER, J. Craig et al.  
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
;; FILE REFERENCE: CLO01307  
;; CURRENT APPLICATION NUMBER: US/09/949,016  
;; PRIOR FILING DATE: 2000-04-14  
;; PRIOR APPLICATION NUMBER: 60/241,755  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 187814  
;; LENGTH: 601  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-187814

Query Match 1.0%; Score 21; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TTTTAAAAAAAATAGA 363  
DB 328 TTTTAAAAAAAATAGA 308

RESULT 13  
US-09-016-434-1156  
;; Sequence 1156, Application US/09016434  
;; Patent No. 6500938  
;; GENERAL INFORMATION:  
;; APPLICANT: Janice Au-Young  
;; APPLICANT: Jeffrey J. Selhammer  
;; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
;; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
;; NUMBER OF SEQUENCES: 1490  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESS: INCYTE PHARMACEUTICALS, INC.  
;; STREET: 3174 PORTER DRIVE  
;; CITY: PALO ALTO  
;; STATE: CALIFORNIA  
;; COUNTRY: USA  
;; ZIP: 94304  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
;; CURRENT APPLICATION DATA:



```

APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1156:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1531982
US-09-016-434-1156

```

```

Query Match      1.0%; Score 21; DB 3; Length 813;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      339 ATATTTTTTTTTTAAAAA 359
Db      479 ATATTTTTTTTTTAAAAA 499

```

```

RESULT 14
US-09-843-472-2
Sequence 2, Application US/09843472
Patent No. 6544783
GENERAL INFORMATION:
APPLICANT: Perera, J. Ranjan
APPLICANT: Lu, Min
TITLE OF INVENTION: Polynucleotide Sequences from Rice
FILE REFERENCE: AKK-103C5XC1
CURRENT APPLICATION NUMBER: US/09/843,472
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/199,870
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 60/217,891
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/218,366
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/227,231
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 60/237,736
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/253,925
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 938
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(938)
OTHER INFORMATION: n = a, c, g, or t.
US-09-843-472-2

```

```

Query Match      1.0%; Score 21; DB 3; Length 938;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      341 ATTTTTTTTTTAAAAAATA 361
Db      185 ATTTTTTTTTTAAAAAATA 205

```

```

RESULT 15
US-09-843-472-2/c
Sequence 2, Application US/09843472
Patent No. 6544783
GENERAL INFORMATION:
APPLICANT: Perera, J. Ranjan
APPLICANT: Lu, Min
TITLE OF INVENTION: Polynucleotide Sequences from Rice
FILE REFERENCE: AKK-103C5XC1
CURRENT APPLICATION NUMBER: US/09/843,472
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/199,870
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 60/217,891
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/218,366
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/227,231
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 60/237,736
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/253,925
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 938
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(938)
OTHER INFORMATION: n = a, c, g, or t.
US-09-843-472-2

```

```

Query Match      1.0%; Score 21; DB 3; Length 938;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      340 TATTTTTTTTTTAAAAAAT 360
Db      205 TATTTTTTTTTTAAAAAAT 185

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Search completed: April 21, 2006, 09:21:42  
Job time : 403 secs

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Db	274	ATATATTGCATCAAACTCTCTTGGATTAATAAAAAATCTTCTAGCTGAACGATGGGTAA	333	
Qy	333	AGAGAGATATTTTTTTTTTAAAAAAAATGAATGAAGATATTTCTGAACGTATCGCAAG	392	
Db	334	AGAGAGATATTTTTTTTTT-----AAAAAATGGAATGAAGATATTTCTGAACGTATCGCAAG	390	
Qy	393	ATTTAACAATATATATATATTAATTTATATGTTTGTGCATTCGTTATATGCGACGTATTA	452	
Db	391	ATTTAACAATATATATATATTAATTTATATGTTTGTGCATTCGTTATATGCGACGTATTA	450	
Qy	451	AGGACATGCTTATCTCCATCTCAATTTTTATTTAGTAAATTAAGAAATTTGACTTATTTT	512	
Db	451	AGGACATGCTTATCTCCATCTCAATTTTTATTTAGTAAATTAAGAAATTTGACTTATTTT	510	
Qy	513	TATTAATTATCTTTTTTTCGATTAGATGCAAGGTACTTACGACACACTTTGTGCTCATGT	572	
Db	511	TATTAATTATCTTTTTTTCGATTAGATGCAAGGTACTTACGACACACTTTGTGCTCATGT	570	
Qy	573	GCATGTGTGATGCGACCTCTCTC-ATACAGTTCAACTACGACACATCTCCAAATACAT	631	
Db	571	GCATGTGTGATGCGACCTCTCTCAATACAGTTCAACTACGACACATCTCTAATATACAT	630	
Qy	632	CGCCTATTTAATACATTTTAGTAGTAGCAATATCTGAATTTCAAGCACTTCAACATCACGAC	691	
Db	631	CGCCTATTTAATACATTTTAGTAGTAGCAATATCTGAATTTCAAGCACTTCAACATCACGAC	690	
Qy	692	CACCTTTAATAAATATCTTAAATAACAAAAATAATTTTACAGATATAGCAATGAATATGA	751	
Db	691	CACCTTTAATAAATATCTTAAATAACAAAAATAATTTTACAGATATAGCAATGAATATGA	750	
Qy	752	AACGAACATTTTAGGTTTTTTCACATACAAAAAAAAGATTTTGTCTGTGCGGAGG	811	
Db	751	AACGAACATTTTAGGTTTTTTCACATACAAAAAAAAGATTTTGTCTGTGCGGAGG	810	
Qy	812	CCAACTCTCCCATATTTGGGCGACACAGGCAACAACAGAGTGGTGGCCACAGAAACAACCCAC	871	
Db	811	CCAACTCTCCCATATTTGGGCGACACAGGCAACAACAGAGTGGTGGCCACAGAAACAACCCAC	870	
Qy	872	AAAAAACGATGATCTTAACCGAGAGACAGC	899	
Db	871	AAAAAACGATGATCTTAACCGAGAGACAGC	898	
RESULT 2				
US-10-012-070A-50				
; Sequence 50, Application US/10012070A				
; Publication No. US20030077801A1				
; GENERAL INFORMATION:				
; APPLICANT: Hawkes, Timothy				
; APPLICANT: Warner, Simon				
; APPLICANT: Andrews, Christopher				
; APPLICANT: Bachoo, Savinder				
; APPLICANT: Pickerill, Andrew				
; TITLE OF INVENTION: Herbicide Resistant Plants				
; FILE REFERENCE: 50490/UST				
; CURRENT APPLICATION NUMBER: US/10/012,070A				
; CURRENT FILING DATE: 2001-10-29				
; PRIOR APPLICATION NUMBER: PCT/GB00/01573				
; PRIOR FILING DATE: 2000-04-20				
; NUMBER OF SEQ ID NOS: 57				
; SOFTWARE: PatentIn Ver. 2.0				
; SEQ ID NO 50				
; LENGTH: 898				
; TYPE: DNA				
; ORGANISM: Oryza sp.				
US-10-012-070A-50				
Qy	18.3%;	Score 402;	DB 5;	Length 898;
	Best Local Similarity	99.3%;	Pred. No. 1.5e-184;	
Matches	862;	Conservative	0;	Mismatches 2;
			Indels	4;
			Gaps	2
Qy	33	CTAACTAAACAATATATGAGAACTGTGCTTAATTAATAATGAAGACTTATATATGTAGCGC	92	

Db 34 CTTAACTAACAAATATATGGGAACGTCGTAAATATAAATATGACCTTAATATATGACGC 93

Qy 93 TGAATACATGAACTATATGTAAGAAAACTCATCACTACTTATGTGGCAATCGGGCTTAA 152

Db 94 TGATTAATGAACTATATGTAAGAAAACTCATCACTACTTATGTGGCAATCGGGCTTAA 153

Qy 153 TAAAAAGAGTGGCTACACTAGTTGCTTTCTTATGTAATTAAGTGGAAAAATGAATC 212

Db 154 TAAAAAGAGTGGCTACACTAGTTGCTTTCTTATGTAATTAAGTGGAAAAATGAATC 213

Qy 213 ATTATTCCTTAGAATAATACGTTACATCTCTGTATGTAAGTAATTAATTCGAGTAGCC 272

Db 214 ATTATTCCTTAGAATAATACGTTACATCTCTGTATGTAAGTAATTAATTCGAGTAGCC 273

Qy 273 ATAAATTCATCAAACTCTTCTGTAATAAAAAATCTTCTAGCTCAACTCAATGGCTAA 333

Db 274 ATAAATTCATCAAACTCTTCTGTAATAAAAAATCTTCTAGCTCAACTCAATGGCTAA 333

Qy 333 AGAGAGATATTTTTTTTTTAAAAAAATGAATGAAGATATTCGTGAACGATCGGCAAG 392

Db 334 AGAGAGATATTTTTTTTTTAAAAAAATGAATGAAGATATTCGTGAACGATCGGCAAG 390

Qy 393 ATTTAAACATATATTAATTAATTTATAGTTTGTGTCATTCGTATATGCAAGTCAATTA 452

Db 391 ATTTAAACATATATTAATTAATTTATAGTTTGTGTCATTCGTATATGCAAGTCAATTA 450

Qy 453 AGACATGCTTTACTCCATCTCAATTTTATTTAGTAATTAAGACAAATGACTATTTT 512

Db 451 AGACATGCTTTACTCCATCTCAATTTTATTTAGTAATTAAGACAAATGACTATTTT 510

Qy 513 TATTTATTAATCTTTTTCGATTAGATGCAAGGACTTACGCACTTGTGCTCATGT 572

Db 511 TATTTATTAATCTTTTTCGATTAGATGCAAGGACTTACGCACTTGTGCTCATGT 570

Qy 573 GCATGTGTGAGTGCACTCTCTC-ATACAGTTCAACTAGCAACACATCTCCATATCACT 631

Db 571 GCATGTGTGAGTGCACTCTCTC-ATACAGTTCAACTAGCAACACATCTCTATATCACT 630

Qy 632 CGCCTATTTAATGCAATTTAGGTAGCAATATCTGAATTCGAACCTTACCATGACCGAC 691

Db 631 CGCCTATTTAATGCAATTTAGGTAGCAATATCTGAATTCGAACCTTACCATGACCGAC 690

Qy 692 CACTTTTAAATATATCTAATAATCAAAAAATTAATTTTACAGAAATACGATAAAGTATGA 751

Db 691 CACTTTTAAATATATCTAATAATCAAAAAATTAATTTTACAGAAATACGATAAAGTATGA 750

Qy 752 AACGAACATTTAAGGTTTTTTCACATACAAAAAAAAGAAATTTGCTGTCGCGAGCG 811

Db 751 AACGAACATTTAAGGTTTTTTCACATACAAAAAAAAGAAATTTGCTGTCGCGAGCG 810

Qy 812 CCAATCTCCATATTTGGGCACACAGGCAACACAGAGTGGCTGCCACAGAACCAATCCAC 871

Db 811 CCAATCTCCATATTTGGGCACACAGGCAACACAGAGTGGCTGCCACAGAACCAATCCAC 870

Qy 872 AAAAAACGATGATCTTAACGAGAGACACG 899

Db 871 AAAAAACGATGATCTTAACGAGAGACACG 898

RESULT 3

US-10-437-963-33718

/ Sequence 33718, Application US/10437963

/ Publication No. US2004012343A1

/ GENERAL INFORMATION:

/ APPLICANT: La Rosa, Thomas J.

/ APPLICANT: Kovalic, David K.

/ APPLICANT: Zhou, Yihua

/ APPLICANT: Cao, Yongwei

/ APPLICANT: Wu, Wei

/ APPLICANT: Boukharov, Andrey A.

/ APPLICANT: Barbasuk, Brad

/ APPLICANT: Li, Ping

/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With



Query Match	3.3%;	Score 73;	DB 7;	Length 808;
Best Local Similarity	100.0%;	Pred. No.	2.3e-24;	

CURRENT FILING DATE: 2003-05-14

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; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 54806
; LENGTH: 213
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_56875C.1
US-10-437-963-54806

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Query Match	2.0%;	Score 44;	DB 7;	Length 213;
Best Local Similarity	100.0%;	Pred. No. 2.9e-10;		
Matches 44;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1023 GGAGGCA TTCACCAAGCAAGAGGGAGACCAAGGACACGCG 1066  
 |||||  
 Db 6 GGAGGCA TTCACCAAGCAAGAGGGAGACCAAGGACACGCG 49

RESULT 10  
US-10-437-963-49995  
COMMUNIST ASSOCIATION FOR THE 100437063

```

Sequence 49995, Application US/10437,963
Publication No. US2004012343A1
GENERAL INFORMATION:
APPLICANT: La Rose, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 49995
LENGTH: 294
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(294)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_52525C.1
US-10-437-963-49995

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Query Match	1.7%	Score 37;	DB 7;	Length 294;
Best Local Similarity	100.0%	Pred. No. 7.6e-07;		
Matches	37;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

Oy	2158	GTTCTTGGTGAGCTTCGACATTTCAACAAGAAATT	2199
Dd	106	GTTCTTGGTGAGCTTCGACATTTCAACAAGAAATT	142

RESULT 11  
 US-10-437-963-7910/c  
 ; Sequence 7910, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovacic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

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: FILE REFERENCE: 38-21(53221)B
: CURRENT APPLICATION NUMBER: US/10/437,963
: CURRENT FILING DATE: 2003-05-14
: NUMBER OF SEQ ID NOS: 204966
: SEQ ID NO 7910
:
: LENGTH: 922

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OTHER INFORMATION: CLONE ID: PAT\_MRT4530\_14461C.1  
US-10-437-963-7910

Query Match	1.7%;	Score 37;	DB 7;	Length 92;
Best Local Similarity	100.0%;	Pred. No. 8e-07;		
Matches 37;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy	2158 GTTCTGTGATAGCTTGCCACTTCACACGAAGTT	2194
Db	894 GTTCTGTGATAGCTTGCCACTTCACACGAAGTT	858

RESULT 12  
US-10-437-963-7903  
Semiannual 7803 and 10010027963

? sequence 7903, Application US/10437903  
 ? Publication No. US20040123343A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: La Rosa, Thomas J.  
 ? APPLICANT: Kovacic, David K.  
 ? APPLICANT: Zhou, Yihua  
 ? APPLICANT: Cao, Yongwei  
 ? APPLICANT: Wu, Wei  
 ? APPLICANT: Boukharov, Andrey A.  
 ? APPLICANT: Barbazuk, Brad  
 ? APPLICANT: Li, Ping  
 ? TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ? TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ? FILE REFERENCE: 38-21(53221)B  
 ? CURRENT APPLICATION NUMBER: US/10/437,963  
 ? CURRENT FILING DATE: 2003-05-14  
 ? NUMBER OF SEQ ID NOS: 204966  
 ? SEQ ID NO 7903  
 ? LENGTH: 2598  
 ? TYPE: DNA  
 ? ORGANISM: *Oryza sativa*  
 ? FEATURE:  
 ? OTHER INFORMATION: Clone ID: PAT\_MRT4530\_14455C.1  
 ? US-10-437-963-7903

Query Match Similarity	1.74;	Score 37;	DB 7;	Length 2598;
Best Local Similarity	100.0%;	Pred. No. 8.3e-07;		
Matches 37;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	2158	GTTCTTGGTGTAGCTTGGCACCCTTTCACACAGCAAGTT	2194
Db	2212	GTTCTTGGTGTAGCTTGGCACCCTTTCACACAGCAAGTT	2248

RESULT 13  
US-10-011-672-14  
Sequence 14, Application US/10011672  
Publication No. US2003004981A1  
GENERAL INFORMATION:  
APPLICANT: Hawkes, Timothy  
APPLICANT: Warner, Simon  
APPLICANT: Andrews, Christopher  
APPLICANT: Bachoo, Satvinder  
APPLICANT: Pickertill, Andrew  
TITLE OR INVENTION: HERBICIDE RESISTANT PLANTS  
FILE REFERENCE: 50489/UST  
CURRENT APPLICATION NUMBER: US/10/011,672  
CURRENT FILING DATE: 2001-10-29  
PRIORITY APPLICATION NUMBER: PCT/GB00/01559  
PRIORITY FILING DATE: 2000-04-20



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/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 14
/ LENGTH: 48
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Primer
US-10-011-672-14
```

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Query Match          1.3%; Score 29; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 AATCCGAAAAGTTCTGCACCGTTTTCAC 29
Db      19 AATCCGAAAAGTTCTGCACCGTTTTCAC 47
```

```
RESULT 14
US-10-012-070A-17
/ Sequence 17, Application US/10012070A
/ Publication No. US20030077801A1
/ GENERAL INFORMATION:
/ APPLICANT: Hawkes, Timothy
/ APPLICANT: Warner, Simon
/ APPLICANT: Andrews, Christopher
/ APPLICANT: Bachoo, Savinder
/ APPLICANT: Pickerill, Andrew
/ TITLE OF INVENTION: Herbicide Resistant Plants
/ FILE REFERENCE: 50490/UST
/ CURRENT APPLICATION NUMBER: US/10/012,070A
/ CURRENT FILING DATE: 2001-10-29
/ PRIOR APPLICATION NUMBER: PCT/GB00/01573
/ PRIOR FILING DATE: 2000-04-20
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 17
/ LENGTH: 48
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:primer
US-10-012-070A-17
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```
Query Match          1.3%; Score 29; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 AATCCGAAAAGTTCTGCACCGTTTTCAC 29
Db      19 AATCCGAAAAGTTCTGCACCGTTTTCAC 47
```

```
RESULT 15
US-10-311-455-63
/ Sequence 63, Application US/10311455
/ Publication No. US20030143606A1
/ GENERAL INFORMATION:
/ APPLICANT: OLEK, Alexander
/ APPLICANT: PIEPENBROCK, Christian
/ APPLICANT: BERLIN, Kurt
/ TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
/ TITLE OF INVENTION: Cytosine methylation
/ FILE REFERENCE: 5013.1014
/ CURRENT APPLICATION NUMBER: US/10/311,455
/ CURRENT FILING DATE: 2002-12-16
/ PRIOR APPLICATION NUMBER: PCT/EP01/07537
/ PRIOR FILING DATE: 2001-07-02
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ PRIOR FILING DATE: 2000-09-01
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/ NUMBER OF SEQ ID NOS: 2424
/ SEQ ID NO 63
/ LENGTH: 12733
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-63
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Query Match          1.2%; Score 27; DB 6; Length 12733;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      333 AGAGAGATATTTTTTTTTTAAAAAAA 359
Db      1915 AGAGAGATATTTTTTTTTTAAAAAAA 1941
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Search completed: April 21, 2006, 10:06:15
Job time : 2647 secs
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GenCore version 5.1.7  
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OM nucleic - nucleic search, using SW model

Run on: April 21, 2006, 09:26:34 ; Search time 5933 Seconds  
(without alignments)  
1497.101 Million cell updates/sec

Title: US-10-541-315-1

Perfect score: 2195  
Sequence: 1 aatccgaaagttctgcac.....catttcaccagcaagttc 2195

Scoring table: OLIGO NEG  
Gapop 60.0, Gapext 60.0

Searched: 9288580 seqs, 2023302648 residues

Word size: 3

Total number of hits satisfying chosen parameters: 18576380

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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2: /SIDSS/ptcodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
3: /SIDSS/ptcodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
4: /SIDSS/ptcodata/1/pubpna/PCR\_NEW\_PUB.seq:\*  
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15: /SIDSS/ptcodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2195	100.0	2195	9	US-10-541-315-1
2	919	41.9	1176	14	US-11-128-548-2
3	750	34.2	1112	14	US-11-128-548-1
4	642	29.2	999	14	US-11-128-548-5
5	22	1.0	378	6	US-09-925-065A-795898
6	22	1.0	567	6	US-09-925-065A-795899
7	22	1.0	660	6	US-09-925-065A-685691
8	22	1.0	1219	6	US-09-925-065A-684849
9	22	1.0	1296	6	US-09-925-065A-92058
10	22	1.0	1296	9	US-10-301-480-193300
11	22	1.0	1296	10	US-10-301-480-806709
12	22	1.0	2195	9	US-10-541-315-1
13	22	1.0	11015	8	US-10-240-708-56
14	22	1.0	151169	14	US-11-121-086-38
15	21	1.0	369	6	US-09-925-065A-110555
16	21	1.0	385	9	US-10-301-480-210061
17	21	1.0	385	10	US-10-301-480-823470
18	21	1.0	474	6	US-09-925-065A-471332

C	19	21	1.0	485	6	US-09-925-065A-471856	Sequence 471856,
C	20	21	1.0	564	10	US-10-301-480-483766	Sequence 483766,
C	21	21	1.0	564	10	US-10-301-480-1097175	Sequence 1097175,
C	22	21	1.0	577	6	US-09-925-065A-743027	Sequence 743027,
C	23	21	1.0	586	6	US-09-925-065A-220810	Sequence 220810,
C	24	21	1.0	603	6	US-09-925-065A-314169	Sequence 314169,
C	25	21	1.0	608	10	US-10-301-480-306237	Sequence 306237,
C	26	21	1.0	608	10	US-10-301-480-919646	Sequence 919646,
C	27	21	1.0	609	10	US-10-301-480-575238	Sequence 575238,
C	28	21	1.0	609	10	US-10-301-480-1188647	Sequence 1188647,
C	29	21	1.0	611	6	US-09-925-065A-733837	Sequence 733837,
C	30	21	1.0	611	6	US-09-925-065A-733838	Sequence 733838,
C	31	21	1.0	611	6	US-09-925-065A-733839	Sequence 733839,
C	32	21	1.0	651	6	US-09-925-065A-256711	Sequence 256711,
C	33	21	1.0	651	6	US-09-925-065A-256712	Sequence 256712,
C	34	21	1.0	651	6	US-09-925-065A-256713	Sequence 256713,
C	35	21	1.0	651	6	US-09-925-065A-256714	Sequence 256714,
C	36	21	1.0	663	10	US-10-301-480-335414	Sequence 335414,
C	37	21	1.0	663	10	US-10-301-480-335415	Sequence 335415,
C	38	21	1.0	663	10	US-10-301-480-335416	Sequence 335416,
C	39	21	1.0	663	10	US-10-301-480-335417	Sequence 335417,
C	40	21	1.0	663	10	US-10-301-480-948823	Sequence 948823,
C	41	21	1.0	663	10	US-10-301-480-948824	Sequence 948824,
C	42	21	1.0	663	10	US-10-301-480-948825	Sequence 948825,
C	43	21	1.0	663	10	US-10-301-480-248826	Sequence 248826,
C	44	21	1.0	839	7	US-10-241-375-51	Sequence 51, Appl
C	45	21	1.0	1737	7	US-10-548-748-29	Sequence 29, Appl

## ALIGNMENTS

RESULT 1									
US-10-541-315-1									
Sequence 1, Application US/10541315									
Publication No. US20060053507A1									
GENERAL INFORMATION:									
APPLICANT: Cropdesign N.V.									
TITLE OF INVENTION: Regulatory sequence									
FILE REFERENCE: CD-072-PCT									
CURRENT APPLICATION NUMBER: US/10/541,315									
CURRENT FILING DATE: 2005-06-30									
PRIOR APPLICATION NUMBER: EP 03075207.5									
PRIOR FILING DATE: 2003-01-21									
NUMBER OF SEQ ID NOS: 3									
SOFTWARE: PatentIn version 3.1									
SEQ ID NO 1									
LENGTH: 2195									
TYPE: DNA									
ORGANISM: Oryza sativa									
US-10-541-315-1									
Query Match									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	1		1	AATCGAAAGTTTGCACCGTTTCACTTAACAATATAGGAGCGTGTCT	60			
DB	1	1	AATCGAAAGTTTGCACCGTTTCACTTAACAATATAGGAGCGTGTCT	60					
QY	61	61		61	AAATATTAAGAGCTTATATATAGCGGTGATTAAGAACTATATAGAAACT	120			
DB	61	61	AAATATTAAGAGCTTATATATAGCGGTGATTAAGAACTATATAGAAACT	120					
QY	121	121		121	CATTCACCTACTTGTGCGCAATCGGCTAATATAAGAGTCCCTACAGTTTGTCT	180			
DB	121	121	CATTCACCTACTTGTGCGCAATCGGCTAATATAAGAGTCCCTACAGTTTGTCT	180					
QY	181	181		181	TTTCCCTGATTAAGTGGGAAATGAATCATTTAGCTAGATATAGCTACATC	240			
DB	181	181	TTTCCCTGATTAAGTGGGAAATGAATCATTTAGCTAGATATAGCTACATC	240					
QY	241	241		241	TCTGTATGAAGTTAAATTAATTCAGGTAGCCATATTTGTCATCAACTCTTGAATA	300			
DB	241	241	TCTGTATGAAGTTAAATTAATTCAGGTAGCCATATTTGTCATCAACTCTTGAATA	300					

Db 241 TCTGTCATGAAAGTTAAATTAATTCAGAGTACGCTAAATTCATCAAACTCTCTTGAAATA 300  
 Qy 301 AAAAAATCTTTAGCTGAACTCAATGGGTAAAGAGATATTTTTTTTTTAAAAAAAT 360  
 Db 301 AAAAAATCTTTAGCTGAACTCAATGGGTAAAGAGATATTTTTTTTTTAAAAAAAT 360  
 Qy 361 AGAATGAGATATTTCTGAAAGTATCGGCAAAAGATTTAAACATTAATTAATTTAT 420  
 Db 361 AGAATGAGATATTTCTGAAAGTATCGGCAAAAGATTTAAACATTAATTAATTTAT 420  
 Qy 421 AGTTTGTGATTCGTTATATCGACGTCAATTAAGACATGCTTACTCATCTCAATTTT 480  
 Db 421 AGTTTGTGATTCGTTATATCGACGTCAATTAAGACATGCTTACTCATCTCAATTTT 480  
 Qy 481 TATTTAGTAATTAAGACATTTGATTTTATTTATTTATTTTCTTTTTCGATTAGATGC 540  
 Db 481 TATTTAGTAATTAAGACATTTGATTTTATTTATTTATTTTCTTTTTCGATTAGATGC 540  
 Qy 541 AAGGTACTTACGACACACTTTGTGCTCATGTGCAATGTGAGTGCACCTCTCATACAC 600  
 Db 541 AAGGTACTTACGACACACTTTGTGCTCATGTGCAATGTGAGTGCACCTCTCATACAC 600  
 Qy 601 GTTCAACTGCGACACATCTCCAAATATCACTGCTCTTAAATACATTTAGTACGAATA 660  
 Db 601 GTTCAACTGCGACACATCTCCAAATATCACTGCTCTTAAATACATTTAGTACGAATA 660  
 Qy 661 TCGAATTCAGACATTCACATCCACAGACACTTTTAAATATCTAAATATCAAAATA 720  
 Db 661 TCGAATTCAGACATTCACATCCACAGACACTTTTAAATATCTAAATATCAAAATA 720  
 Qy 721 ATATTTTACAGATAGCATGAAAGATGAAAGATGAAAGATTTAGGTTTTTTCATACAA 780  
 Db 721 ATATTTTACAGATAGCATGAAAGATGAAAGATGAAAGATTTAGGTTTTTTCATACAA 780  
 Qy 781 AAAAAAAGATTTTGTCTGTGCGGAGCGCAATCTCCCATTTGGGACACAGGCA 840  
 Db 781 AAAAAAAGATTTTGTCTGTGCGGAGCGCAATCTCCCATTTGGGACACAGGCA 840  
 Qy 841 CAACAGAGTGGCTGCCACAGAACCAACCAAAACATGATCTTAACGAGAGACAGA 900  
 Db 841 CAACAGAGTGGCTGCCACAGAACCAACCAAAACATGATCTTAACGAGAGACAGA 900  
 Qy 901 AGTCCGCAACACTTTTAAACAGCAGCTTTGCGGCAGAGAGAGAGAGAGGCAAG 960  
 Db 901 AGTCCGCAACACTTTTAAACAGCAGCTTTGCGGCAGAGAGAGAGAGAGGCAAG 960  
 Qy 961 AAAAAAGATTCCTCTCTCCATCTTAATAATTCCTCCCTTTTCCCTCTCTATA 1020  
 Db 961 AAAAAAGATTCCTCTCTCCATCTTAATAATTCCTCCCTTTTCCCTCTCTATA 1020  
 Qy 1021 TAGGAGGATTCAGACCAAGGAGAGAGAGACCAAGGACAGGCACTAGCAGAACCG 1080  
 Db 1021 TAGGAGGATTCAGACCAAGGAGAGAGAGAGACCAAGGACAGGCACTAGCAGAACCG 1080  
 Qy 1081 AGCGACCGGCTTCTGATCTCATATCTTCGATCGATCTCTGATCTCTCCCTCC 1140  
 Db 1081 AGCGACCGGCTTCTGATCTCATATCTTCGATCGATCTCTGATCTCTCCCTCC 1140  
 Qy 1141 TCCACTCTCTCTCACAGGATATGCTGCTGCTTCTTGATTTATGTTCTAGGT 1200  
 Db 1141 TCCACTCTCTCTCACAGGATATGCTGCTGCTTCTTGATTTATGTTCTAGGT 1200  
 Qy 1201 TGTGTAGTACGGGCGTTGATGTTAGGAGAGGGAATGATCTGATGATTTCTGTTCT 1260  
 Db 1201 TGTGTAGTACGGGCGTTGATGTTAGGAGAGGGAATGATCTGATGATTTCTGTTCT 1260  
 Qy 1261 TGGATTTGGGATAGAGGGGTTCTTGAATGTTGATCTGATCTGATTTGATTTAGTACT 1320  
 Db 1261 TGGATTTGGGATAGAGGGGTTCTTGAATGTTGATCTGATCTGATTTGATTTAGTACT 1320  
 Qy 1321 ATGCTTTCAATCGCTTGAGAGCTCTATGAAATGAAATGTTTAGGCTACGGAATCTT 1380  
 Db 1321 ATGCTTTCAATCGCTTGAGAGCTCTATGAAATGAAATGTTTAGGCTACGGAATCTT 1380

Db 1321 ATGCTTTCAATCGCTTGAGAGCTCTATGAAATGAAATGTTTAGGCTACGGAATCTT 1380  
 Qy 1381 GCGATTTGTGAGTACCTTTTGTGAGTAAATCAAGACACCGGTATTTGCTGTGT 1440  
 Db 1381 GCGATTTGTGAGTACCTTTTGTGAGTAAATCAAGACACCGGTATTTGCTGTGT 1440  
 Qy 1441 GTATTAAGATGATTTGTTGTGCTGATTTCTGTGTGTATGCTTTCTGATTTGAGCA 1500  
 Db 1441 GTATTAAGATGATTTGTTGTGCTGATTTCTGTGTGTATGCTTTCTGATTTGAGCA 1500  
 Qy 1501 AGCTATCCCTTTGTTATTTCCCTATGAAACAAAATATCAAACTTTGAAAGACGCTCCGT 1560  
 Db 1501 AGCTATCCCTTTGTTATTTCCCTATGAAACAAAATATCAAACTTTGAAAGACGCTCCGT 1560  
 Qy 1561 TGATGAGATGTAATGATTTGATTTTACGCTGTCMAAATTTTCCGAGCTGCTGTGTAG 1620  
 Db 1561 TGATGAGATGTAATGATTTGATTTTACGCTGTCMAAATTTTCCGAGCTGCTGTGTAG 1620  
 Qy 1621 ATACAGTATGCTCCCATCAAGAAATTCATGAAACAGTTATATCTCAGAAACAGGGAT 1680  
 Db 1621 ATACAGTATGCTCCCATCAAGAAATTCATGAAACAGTTATATCTCAGAAACAGGGAT 1680  
 Qy 1681 TCCCTGTTCTCCGATTTGCTTATGCTCCAGAAATTTTTCCTCAAAATATCTTAAAGT 1740  
 Db 1681 TCCCTGTTCTCCGATTTGCTTATGCTCCAGAAATTTTTCCTCAAAATATCTTAAAGT 1740  
 Qy 1741 CACTTTCTGTTCACTTCAATGAAATGATTTGCTACAAATATGCTTTATAGCGTTATCC 1800  
 Db 1741 CACTTTCTGTTCACTTCAATGAAATGATTTGCTACAAATATGCTTTATAGCGTTATCC 1800  
 Qy 1801 TAGCTGTAGTCACTTATAGTATATACCTCTATAGTTTATGTCAGAGAGAAAGATTTACC 1860  
 Db 1801 TAGCTGTAGTCACTTATAGTATATACCTCTATAGTTTATGTCAGAGAGAAAGATTTACC 1860  
 Qy 1861 GATTTCTGATCCATTTTATTTATTTATGAAATGAAATGATGATGATGATGATGATGAT 1920  
 Db 1861 GATTTCTGATCCATTTTATTTATTTATGAAATGAAATGATGATGATGATGATGATGAT 1920  
 Qy 1921 GGATTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1980  
 Db 1921 GGATTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1980  
 Qy 1981 ACTGCTGCAATTTTGTGTTTCAATTCACATGATTTATCTGATTTATCTCTGTATC 2040  
 Db 1981 ACTGCTGCAATTTTGTGTTTCAATTCACATGATTTATCTGATTTATCTCTGTATC 2040  
 Qy 2041 TACCTGTAGAGTTCTTTTGTGTTATCTTGAATGATTTATCTGATTTATCTCTGTATC 2100  
 Db 2041 TACCTGTAGAGTTCTTTTGTGTTATCTTGAATGATTTATCTGATTTATCTCTGTATC 2100  
 Qy 2101 GAACTGTATTCGAGATGATTTATCTGTTGTTTATGATTTATCTGTTGTTGTTGTTGTTGTT 2160  
 Db 2101 GAACTGTATTCGAGATGATTTATCTGTTGTTTATGATTTATCTGTTGTTGTTGTTGTTGTT 2160  
 Qy 2161 CTGCTGTAGCTTCCACTTTCACCAAGATTC 2195  
 Db 2161 CTGCTGTAGCTTCCACTTTCACCAAGATTC 2195

RESULT 2  
 US-11-128-549-2  
 / Sequence 2, Application US/11128549  
 / Publication No. US20050262597A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Broekaert, Willem  
 / APPLICANT: De Wilde, Chris  
 / APPLICANT: Hatfeld, Yves  
 / APPLICANT: Zhou, Zhongyi  
 / TITLE OF INVENTION: METHOD FOR INCREASING TRANSGENE EXPRESSION  
 / FILE REFERENCE: 1187-40  
 / CURRENT APPLICATION NUMBER: US/11/128,549  
 / PRIORITY FILING DATE: 2005-05-13  
 / PRIOR APPLICATION NUMBER: US 60/572,141



Db	306	GGAACTCTTGCAGTTTTTGAGTACTTTTGTTTAGAGTAAATCAGAGCACCGGTGATTT	365
Qy	1433	TGCTTGTGTATATAAAGTACATTTGTTGGTCTCGATTCGTGTAGTATGCTTCTCGA	1492
Db	366	TGCTTGTGTATATAAAGTACAGGTGTTTGGTCCCTCGATTCGTGTAGTATGCTTCTCGA	425
Qy	1493	TTTGAACGAAGCTATCCTTGTGTTATTTCCCTATGTAAACAAAATATATCCACTTTGGAAGAC	1552
Db	426	TTTGAACGAAGCTATCCTTGTGTTATTTCCCTATGTAAACAAAATATATCCACTTTGGAAGAC	485
Qy	1553	GGTCCCGTTGATAGATAGAAATGATTTGATTCCTTAAGCCTGTCCAAAATTTTGCAGCTGGC	1612
Db	486	GGTCCCGTTGATAGATAGAAATGATTTGATTCCTTAAGCCTGTCCAAAATTTTGCAGCTGGC	545
Qy	1613	TTGTTTAGATACAGTAGTCCCATCAGCAAAATTCATGTAAAACAGTTATATCTCAGGAA	1672
Db	546	TTGTTTAGATACAGTAGTCCCATCAGCAAAATTCATGTAAAACAGTTATATCTCAGGAA	605
Qy	1673	CAGGGGATTCCTCGTGTCTTCCGATTTGCTTATGTCCAGAAATTTTTTTTCCCAAAATCT	1732
Db	606	CAGGGGATTCCTCGTGTCTTCCGATTTGCTTATGTCCAGAAATTTTTTTTCCCAAAATCT	665
Qy	1733	TAAAAAGCACATTTCTGGTTTCAGTTCATGAAATGATTCGTAACAATATGCTTTTATAG	1792
Db	666	TAAAAAGCACATTTCTGGTTTCAGTTCATGAAATGATTCGTAACAATATGCTTTTATAG	725
Qy	1793	CGTATCTCAGCTGTAGTTCAATTATAGTAAATCCCTATAGTTTATGTACAGAGAGA	1852
Db	726	CGTATCTCAGCTGTAGTTCAATTATAGTAAATCCCTATAGTTTATGTACAGAGAGA	785
Qy	1853	ACTATCCGATTTCTGATCTCCATTTTAAATATAGAAATGAACCTGTAGCATACAGCT	1912
Db	786	ACTATCCGATTTCTGATCTCCATTTTAAATATAGAAATGAACCTGTAGCATACAGCT	845
Qy	1913	ATTCAATTGGAATATTTTTTTTATTAAGCTTCACCCCCTCATTTATTCGACCTGAAAGTC	1972
Db	846	ATTCAATTGGAATATTTTTTTTATTAAGCTTCACCCCCTCATTTATTCGACCTGAAAGTC	905
Qy	1973	TGGCATGAACTGCTCTCAATTTGTTTTCAATTCACATCGATTAATCATGATTAATCT	2032
Db	906	TGGCATGAACTGCTCTCAATTTGTTTTCAATTCACATCGATTAATCATGATTAATCT	965
Qy	2033	CTGTATCTACCTGTAGAAAGTTCTTTTGGTTATTCCTTGAAGCTGTGATTAACAAG	2092
Db	966	CTGTATCTACCTGTAGAAAGTTCTTTTGGTTATTCCTTGAAGCTGTGATTAACAAG	1025
Qy	2093	AAATTATGAAGCTGTAAATCGGAATAGTTATCTGCTGTTCTTATGATTAATTCCTTT	2152
Db	1026	AAATTATGAAGCTGTAAATCGGAATAGTTATCTGCTGTTCTTATGATTAATTCCTTT	1085
Qy	2153	GTGCAGTCTGTGTAGCTTGCCACT	2179
Db	1086	GTGCAGTCTGTGTAGCTTGCCACT	1112

RESULT 4  
US-11-128-549-5  
Sequence 5, Application US/11128549  
Publication No. US20050262597A1  
GENERAL INFORMATION:  
APPLICANT: Broekaert, Willem  
APPLICANT: De Wilde, Chris  
APPLICANT: Hatzfeld, Yves  
APPLICANT: Zhou, Zhongyi  
TITLE OF INVENTION: METHOD FOR INCREASING TRANSGENE EXPRESSION  
FILE REFERENCE: 1187-40  
CURRENT APPLICATION NUMBER: US/11/128, 549  
CURRENT FILING DATE: 2005-05-13  
PRIOR APPLICATION NUMBER: US 60/572,141  
PRIOR FILING DATE: 2004-05-18  
PRIOR APPLICATION NUMBER: EP 04102108.0  
PRIOR FILING DATE: 2004-05-13

; NUMBER OF SEQ ID NOS: 5									
; SOFTWARE: Patentin version 3.2									
; SEQ ID NO 5									
; LENGTH: 999									
; TYPE: DNA									
; ORGANISM: Oryza sativa									
us-11-128-549-5									
Query Match 29.2%; Score 642; DB 14; Length 999;									
Best Local Similarity 99.3%; Pred. No. 2e-275;									
Matches 992; Conservative 0; Mismatches 7; Indels 0; Gaps 0;									
Oy	1160	GTATGTGCGCCCTCGATTGTTCTTGGAATTTATGTTCTTCAGTGTGTGTAGTACGCGCGTTGA	1219						
Ds	1	GTAATGTCCCTTCGCTGTTCTTGGAATTTATGTTCTTCAGTGTGTGTAGTACGCGCGTTGA	60						
Oy	1220	TGTTAGGAAAGGGGATCTGATCTGTGATGATTCCTGTTCTTGATTTGGATAGAGGG	1279						
Ds	61	TGTTAGGAAAGGGGATCTGATCTGTGATGATTCCTGTTCTTGATTTGGATAGAGGG	120						
Oy	1280	TTCTTGATGTGCATGTTATCGGTTCCGTTTGATTTAGTATGATGTTTCAATGCTCTGG	1332						
Ds	121	TTCTTGATGTGCATGTTATCGGTTCCGTTTGATTTAGTATGATGTTTCAATGCTCTGG	180						
Oy	1340	AGACCTCATGGAATGAAATGTTTGGGTAACGGAATCTGGCATTTTGAGATCCTT	1399						
Ds	181	AGACCTCATGGAATGAAATGTTTGGGTAACGGAATCTGGCATTTTGAGATCCTT	240						
Oy	1400	TTGTTTGGAGTAATCAGACACCGGTGATTTTGCTGTGTATATAAAGTACATTTGT	1458						
Ds	241	TTGTTTGGAGTAATCAGACACCGGTGATTTTGCTGTGTATATAAAGTACATTTGT	300						
Oy	1460	TTGGTCTCGATTCGGTAGTGATGCTTCTCGATTTGACGAAGCTATCCTTTGTTATTC	1519						
Ds	301	TTGGTCTCGATTCGGTAGTGATGCTTCTCGATTTGACGAAGCTATCCTTTGTTATTC	360						
Oy	1520	CCATTTGGAACAAATAATCCAACTTTGAGAAGCGTCCCGTTGATGGAATTGAATGATTG	1579						
Ds	361	CCATTTGGAACAAATAATCCAACTTTGAGAAGCGTCCCGTTGATGGAATTGAATGATTG	420						
Oy	1580	ATTCTTAAGCTGTGCCAAATTTTGGCAGCTGGTGTATTAGATACAGTAGTCCCATCAC	1638						
Ds	421	ATTCTTAAGCTGTGCCAAATTTTGGCAGCTGGTGTATTAGATACAGTAGTCCCATCAC	480						
Oy	1640	GAAATTCATGAAAACAGTTATTAATCTTCAGGAACAGGGGATTCCTGTTCTTCGATTTG	1699						
Ds	481	GAAATTCATGAAAACAGTTATTAATCTTCAGGAACAGGGGATTCCTGTTCTTCGATTTG	540						
Oy	1700	CTTTAGTCCCGAATTTTTTTCCTCAATATCTTAAAGACATCTTCGTTCACTTCA	1758						
Ds	541	CTTTAGTCCCGAATTTTTTTCCTCAATATCTTAAAGACATCTTCGTTCACTTCA	600						
Oy	1760	ATGAATGATTGCTACAAATAATGCTTTTATAGGCTTATCTAGCTGATTCAGTTAT	1819						
Ds	601	ATGAATGATTGCTACAAATAATGCTTTTATAGGCTTATCTAGCTGATTCAGTTAT	660						
Oy	1820	AGGTAAATACCCCTATAGTTTATGTCAGAGAAAGAACTTATCCGATTTCTGATCTCCATTTT	1879						
Ds	661	AGGTAAATACCCCTATAGTTTATGTCAGAGAAAGAACTTATCCGATTTCTGATCTCCATTTT	720						
Oy	1880	TAAATTATATGAATGAAGTGTAGCATAGCATGATTCATTTGGATATTTTTTTTATATAG	1933						
Ds	721	TAAATTATATGAATGAAGTGTAGCATAGCATGATTCATTTGGATATTTTTTTTATATAG	780						
Oy	1940	CTTTCACCCCTCATTTATCTGACCTGAAAGCTGGGATGAACTGCTCAATTTGTTT	1999						
Ds	781	CTTTCACCCCTCATTTATCTGACCTGAAAGCTGGGATGAACTGCTCAATTTGTTT	840						
Oy	2000	TCAATTCACATCGATTTATCTAGTATTCCTCTTGATCTTACCTGTAGAAAGTTCTTT	2055						
Ds	841	TCAATTCACATCGATTTATCTAGTATTCCTCTTGATCTTACCTGTAGAAAGTTCTTT	900						
Oy	2060	TTGGTATTCCTTGACGTGATTTACAGAAAGAAATTTATGAAGCTGTAATCCGGATAG	2115						

```
Db      901 TTGGTATTCCTGACGCTGATTAACAAGAAATTTATGAAGCTGATATCGGATAG 960
Qy      2120 TTAACTGCTGTTCTTATGATTCATTTCTTGTGCG 2158
        |||||||
Db      961 TTATAGCTGTTGTTCTTATGATTCATTTCTTGTGCG 999
```

## RESULT 5

```
US-09-925-065A-795898/c
; Sequence 795898, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 795898
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-795898
```

```
Query Match      1.0%; Score 22; DB 6; Length 378;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      772 CACATACAAAAAAGAAAT 793
        |||||||
Db      353 CACATACAAAAAAGAAAT 332
```

## RESULT 6

```
US-09-925-065A-795899/c
; Sequence 795899, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 795899
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
US-09-925-065A-795899
```

```
Query Match      1.0%; Score 22; DB 6; Length 567;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      772 CACATACAAAAAAGAAAT 793
        |||||||
Db      223 CACATACAAAAAAGAAAT 202
```

## RESULT 7

```
US-09-925-065A-685691/c
; Sequence 685691, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 685691
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-685691
```

```
Query Match      1.0%; Score 22; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      337 AGATATTTTTTTTAAAAAAA 358
        |||||||
Db      198 AGATATTTTTTTTAAAAAAA 177
```

## RESULT 8

```
US-09-925-065A-684849
; Sequence 684849, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 684849
```

/ LENGTH: 1219  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
US-09-925-065A-684849

Query Match 1.0%; Score 22; DB 6; Length 1219;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 779 AAAAAAAAAAGATTGCTC 800  
|||||  
Db 612 AAAAAAAAAAGATTGCTC 633

RESULT 9  
US-09-925-065A-92058/c  
/ Sequence 92058, Application US/09925065A  
/ Publication No. US20040181048A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Wang, David G.  
/ TITLE OF INVENTION: Identification and Mapping of Single  
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
/ FILE REFERENCE: 108827.135  
/ CURRENT APPLICATION NUMBER: US/09/925,065A  
/ PRIOR FILING DATE: 2001-08-08  
/ PRIOR APPLICATION NUMBER: US 60/243,096  
/ PRIOR FILING DATE: 2000-10-24  
/ PRIOR APPLICATION NUMBER: US 60/252,147  
/ PRIOR FILING DATE: 2000-11-20  
/ PRIOR APPLICATION NUMBER: US 60/250,092  
/ PRIOR FILING DATE: 2000-11-30  
/ PRIOR APPLICATION NUMBER: US 60/261,766  
/ PRIOR FILING DATE: 2001-01-16  
/ PRIOR APPLICATION NUMBER: US 60/289,846  
/ PRIOR FILING DATE: 2001-05-09  
/ NUMBER OF SEQ ID NOS: 957086  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 92058  
/ LENGTH: 1296  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
US-09-925-065A-92058

Query Match 1.0%; Score 22; DB 6; Length 1296;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 772 CACATACAAAAAAAAAGAT 793  
|||||  
Db 223 CACATACAAAAAAAAAGAT 202

RESULT 10  
US-10-301-480-193300/c  
/ Sequence 193300, Application US/10301480  
/ Publication No. US20060057564A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Wang, David G.  
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
/ TITLE OF INVENTION: In the Human Genome  
/ FILE REFERENCE: 108827.137  
/ CURRENT APPLICATION NUMBER: US/10/301,480  
/ PRIOR FILING DATE: 2002-11-21  
/ PRIOR APPLICATION NUMBER: US 10/215,598  
/ PRIOR FILING DATE: 2002-08-09  
/ PRIOR APPLICATION NUMBER: US 60/311,695  
/ PRIOR FILING DATE: 2001-08-10  
/ NUMBER OF SEQ ID NOS: 1226818  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 193300  
/ LENGTH: 1296  
/ TYPE: DNA  
/ ORGANISM: Homo sapien

US-10-301-480-193300

Query Match 1.0%; Score 22; DB 9; Length 1296;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 772 CACATACAAAAAAAAAGAT 793  
|||||  
Db 223 CACATACAAAAAAAAAGAT 202

RESULT 11  
US-10-301-480-806709/c  
/ Sequence 806709, Application US/10301480  
/ Publication No. US20060057564A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Wang, David G.  
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
/ TITLE OF INVENTION: In the Human Genome  
/ FILE REFERENCE: 108827.137  
/ CURRENT APPLICATION NUMBER: US/10/301,480  
/ PRIOR FILING DATE: 2002-11-21  
/ PRIOR APPLICATION NUMBER: US 10/215,598  
/ PRIOR FILING DATE: 2002-08-09  
/ PRIOR APPLICATION NUMBER: US 60/311,695  
/ PRIOR FILING DATE: 2001-08-10  
/ NUMBER OF SEQ ID NOS: 1226818  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 806709  
/ LENGTH: 1296  
/ TYPE: DNA  
/ ORGANISM: Homo sapien  
US-10-301-480-806709

Query Match 1.0%; Score 22; DB 10; Length 1296;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 772 CACATACAAAAAAAAAGAT 793  
|||||  
Db 223 CACATACAAAAAAAAAGAT 202

RESULT 12  
US-10-541-315-1/c  
/ Sequence 1, Application US/10541315  
/ Publication No. US20060053507A1  
/ GENERAL INFORMATION:  
/ APPLICANT: CropDesign N.V.  
/ TITLE OF INVENTION: Regulatory sequence  
/ FILE REFERENCE: CD-072-PC7  
/ CURRENT APPLICATION NUMBER: US/10/541,315  
/ PRIOR FILING DATE: 2005-06-30  
/ PRIOR APPLICATION NUMBER: EP 03075207.5  
/ PRIOR FILING DATE: 2003-01-21  
/ NUMBER OF SEQ ID NOS: 3  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 1  
/ LENGTH: 2195  
/ TYPE: DNA  
/ ORGANISM: Oryza sativa  
US-10-541-315-1

Query Match 1.0%; Score 22; DB 9; Length 2195;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 340 TATTTTTTTTTTAAAAAATA 361  
|||||  
Db 361 TATTTTTTTTTTAAAAAATA 340

RESULT 13



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US-10-240-708-56/c
; Sequence 56, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPERROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 56
; LENGTH: 11015
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-56

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 700 ATATATCTAAATACAAAAA 721
DB 2698 ATATATCTAAATACAAAAA 2677

RESULT 14
US-11-121-086-38/c
; Sequence 38, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 151169
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-38

Query Match
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 AGATATTTTTTTTTAAAAAAA 358
DB 107567 AGATATTTTTTTTTAAAAAAA 107546

RESULT 15
US-09-925-065A-110555/c
; Sequence 110555, Application US/09925065A
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; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110555
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-110555

Query Match
Best Local Similarity 1.0%; Score 21; DB 6; Length 369;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 339 ATATTTTTTTTTTTTTAAAAAAA 359
DB 183 ATATTTTTTTTTTTTTAAAAAAA 163
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Search completed: April 21, 2006, 11:25:53  
Job time : 5934 secs

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